



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Stojiljkovic, Igor
So, Magdalene
Hwa, Vivian
Heffron, Fred
Nassif, Xavier

(ii) TITLE OF INVENTION: Novel Bacterial Hemoglobin Receptor
Genes and Uses

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
(B) STREET: 300 South Wacker Drive, 32nd Floor
(C) CITY: Chicago
(D) STATE: Illinois
(E) COUNTRY: USA
(F) ZIP: 60606

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/537,361
(B) FILING DATE: 02-OCT-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Noonan, Kevin E
(B) REGISTRATION NUMBER: 35,303
(C) REFERENCE/DOCKET NUMBER: 94,784-A

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 312-913-0001
(B) TELEFAX: 312-913-0002

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 471..2848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGAACTAGTG GATCCAATTT GGGCGCGGCG TTTTGTTC A	AACACGCCCA AAAACTCGAT	60
TACAACGGCG AACACGGCGC GCGCCACCTC GCTCCGCATC	CCGACGGGCC GCGGCAAACA	120
CTGGCGCGCC TTCGTCGAGC ATCTTGAACG CTTTGAACCT	GACTCCCGAA GCCGAAGCGG	180
AAGCCATTCA AGGCGCGCGC GAAGCCTTTG CATTCTACAA	AGTCGTGTTG CGCGAAACCT	240
TCGGCTTGGC AGCCGATGCC GAAGCCCCCG AAGGTATGAT	GCCGCACAGG CACTAAAAAA	300
TAATCGAACC AAATAAACAA GGTCTCGGCA TAGCTGTTTG	CAGGGACCTT TAATTACAG	360
GCGCGGCTTT GTTTACATGG ATTACTGTCT TATTAAATAT	TAATGATTAT CATAAAATCT	420
ATTATTCGCT AACCGATGGA TGAACAATCC ATACATCTTG	AGTTGATAAT ATG AAA	476
	Met Lys	
	1	
CCA TTA CAA ATG CTC CCT ATC GCC GCG CTG GTC	GGC AGT ATT TTC GGC	524
Pro Leu Gln Met Leu Pro Ile Ala Ala Leu Val	Gly Ser Ile Phe Gly	
5	10 15	
AAT CCG GTC TTT GCG GCA GAT GAA GCT GCA ACT	GAA ACC ACA CCC GTT	572
Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr	Glu Thr Thr Pro Val	
20	25 30	
AAG GCA GAG GTA AAA GCA GTG CGC GGT AAA GGC	CAG CGC AAT GCG CCT	620
Lys Ala Glu Val Lys Ala Val Arg Gly Lys Gly	Gln Arg Asn Ala Pro	
35	40 45 50	
GCG GCT GTG GAA CGC GTC AAC CTT AAC CGT ATC	AAA CAA GAA ATG ATA	668
Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile	Lys Gln Glu Met Ile	
55	60 65	
CGC GAC AAC AAA GAC TTG GTG CGC TAT TCC ACC	GAT GTC GGC TTG AGC	716
Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr	Asp Val Gly Leu Ser	
70	75 80	
GAC AGC GGC CGC CAT CAA AAA GGC TTT GCT GTT	CGC GGC GTG GAA GGC	764
Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val	Arg Gly Val Glu Gly	
85	90 95	
AAC CGT GTC GGC GTG AGC ATA GAC GGC GTA AAC	CTG CCT GAT TCC GAA	812
Asn Arg Val Gly Val Ser Ile Asp Gly Val Asn	Leu Pro Asp Ser Glu	
100	105 110	
GAA AAC TCG CTG TAC GCC CGT TAT GGC AAC TTC	AAC AGC TCG CGT CTG	860
Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe	Asn Ser Ser Arg Leu	
115	120 125 130	
TCT ATC GAC CCC GAA CTC GTG CGC AAC ATC GAC	ATC GTA AAA GGG GCG	908
Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Asp	Ile Val Lys Gly Ala	
135	140 145	
GAC TCT TTC AAT ACC GGC AGC GGC GCC TTG GGC	GGC GGT GTG AAT TAC	956
Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly	Gly Gly Val Asn Tyr	
150	155 160	

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Cont

CAA ACC CTG CAA GGA CGT GAC TTA CTG TTG CCT GAA CGG CAG TTC GGC Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Pro Glu Arg Gln Phe Gly 165 170 175	1004
GTG ATG ATG AAA AAC GGT TAC AGC ACG CGT AAC CGT GAA TGG ACA AAT Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp Thr Asn 180 185 190	1052
ACC CTC GGT TTC GGC GTG AGC AAC GAC CGC GTG GAT GCC GCT TTG CTG Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala Leu Leu 195 200 205 210	1100
TAT TCG CAA CGG CGC GGC CAT GAA ACT GAA AGC GCG GGC AAG CGT GGT Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Lys Arg Gly 215 220 225	1148
TAT CCG GTA GAG GGT GCT GGT AGC GGA GCG AAT ATC CGT GGT TCT GCG Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Asn Ile Arg Gly Ser Ala 230 235 240	1196
CGC GGT ATT CCT GAT CCG TCC CAA CAC AAA TAC CAC AGC TTC TTG GGT Arg Gly Ile Pro Asp Pro Ser Gln His Lys Tyr His Ser Phe Leu Gly 245 250 255	1244
AAG ATT GCT TAT CAA ATC AAC GAC AAC CAC CGC ATC GGC GCA TCG CTC Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly Ala Ser Leu 260 265 270	1292
AAC GGT CAG CAG GGG CAT AAT TAC ACG GTT GAA GAG TCT TAC AAC CTG Asn Gly Gln Gln Gly His Asn Tyr Thr Val Glu Glu Ser Tyr Asn Leu 275 280 285 290	1340
CTT GCT TCT TAT TGG CGT GAA GCT GAC GAT GTC AAC AGA CGG CGT AAC Leu Ala Ser Tyr Trp Arg Glu Ala Asp Asp Val Asn Arg Arg Arg Asn 295 300 305	1388
ACC AAC CTC TTT TAC GAA TGG ACG CCG GAA TCC GAC CGG TTG TCT ATG Thr Asn Leu Phe Tyr Glu Trp Thr Pro Glu Ser Asp Arg Leu Ser Met 310 315 320	1436
GTA AAA GCG GAT GTC GAT TAT CAA AAA ACC AAA GTA TCT GCG GTC AAC Val Lys Ala Asp Val Asp Tyr Gln Lys Thr Lys Val Ser Ala Val Asn 325 330 335	1484
TAC AAA GGT TCG TTC CCG ATA GAG GAT TCT TCC ACC TTG ACA CGT AAC Tyr Lys Gly Ser Phe Pro Ile Glu Asp Ser Ser Thr Leu Thr Arg Asn 340 345 350	1532
TAC AAT CAA AAG GAC TTG GAT GAA ATC TAC AAC CGC AGT ATG GAT ACC Tyr Asn Gln Lys Asp Leu Asp Glu Ile Tyr Asn Arg Ser Met Asp Thr 355 360 365 370	1580
CGC TTC AAA CGC ATT ACC CTG CGT TTG GAC AGC CAT CCG TTG CAA CTC Arg Phe Lys Arg Ile Thr Leu Arg Leu Asp Ser His Pro Leu Gln Leu 375 380 385	1628
GGG GGG GGG CGA CAC CGC CTG TCG TTT AAA ACT TTC GCC AGC CGC CGT Gly Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Ala Ser Arg Arg 390 395 400	1676

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Cont

390	395	400	
GAT TTT GAA AAC CTA AAC CGC GAC GAT TAT TAC TTC AGC GGC CGT GTT Asp Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Gly Arg Val 405 410 415			1724
GTT CGA ACC ACC AGC AGT ATC CAG CAT CCG GTG AAA ACC ACC AAC TAC Val Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr Asn Tyr 420 425 430			1772
GGT TTC TCA CTG TCT GAC CAA ATT CAA TGG AAC GAC GTG TTC AGT AGC Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser Ser 435 440 445 450			1820
CGC GCA GGT ATC CGT TAC GAT CAT ACC AAA ATG ACG CCT CAG GAA TTG Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu Leu 455 460 465			1868
AAT GCC GAG TGT CAT GCT TGT GAC AAA ACA CCG CCT GCA GCC AAC ACT Asn Ala Glu Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn Thr 470 475 480			1916
TAT AAA GGC TGG AGC GGT TTT GTC GGC TTG GCG GCG CAA CTG AAT CAG Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Asn Gln 485 490 495			1964
GCT TGG CGT GTC GGT TAC GAC ATT ACT TCC GGC TAC CGT GTC CCC AAT Ala Trp Arg Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val Pro Asn 500 505 510			2012
GCG TCC GAA GTG TAT TTC ACT TAC AAC CAC GGT TCG GGT AAT TGG CTG Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn Trp Leu 515 520 525 530			2060
CCC AAT CCC AAC CTG AAA GCC GAG CGC ACG ACC ACC CAC ACC CTC TCT Pro Asn Pro Asn Leu Lys Ala Glu Arg Thr Thr Thr His Thr Leu Ser 535 540 545			2108
CTG CAA GGC CGC AGC GAA AAA GGT ACT TTG GAT GCC AAC CTG TAT CAA Leu Gln Gly Arg Ser Glu Lys Gly Thr Leu Asp Ala Asn Leu Tyr Gln 550 555 560			2156
AGC AAT TAC CGC AAT TTC CTG TCT GAA GAG CAG AAG CTG ACC ACC AGC Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr Thr Ser 565 570 575			2204
GGC GAT GTC AGC TGT ACT CAG ATG AAT TAC TAC TAC GGT ATG TGT AGC Gly Asp Val Ser Cys Thr Gln Met Asn Tyr Tyr Tyr Gly Met Cys Ser 580 585 590			2252
AAT CCT TAT TCC GAA AAA CTG GAA TGG CAG ATG CAA AAT ATC GAC AAG Asn Pro Tyr Ser Glu Lys Leu Glu Trp Gln Met Gln Asn Ile Asp Lys 595 600 605 610			2300
GCC AGA ATC CGC GGT ATC GAG CTG ACG GGC CGT CTG AAT GTG GAC AAA Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val Asp Lys 615 620 625			2348

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cont

GTA GCG TCT TTT GTT CCT GAG GGC TGG AAA CTG TTC GGC TCG CTG GGT Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu Gly 630 635 640	2396
TAT GCG AAA AGC AAA CTG TCG GGC GAC AAC AGC CTG CTG TTC ACC CAG Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Phe Thr Gln 645 650 655	2444
CCG TTG AAA GTG ATT GCC GGT ATC GAC TAT GAA AGT CCG AGC GAA AAA Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu Lys 660 665 670	2492
TGG GGC GTG TTC TCC CGC CTG ACC TAT CTG GGC GCG AAA AAG GTC AAA Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val Lys 675 680 685 690	2540
GAC GCG CAA TAC ACC GTT TAT GAA AAC AAG GGC TGG GGT ACG CCT TTG Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr Pro Leu 695 700 705	2588
CAG AAA AAG GTA AAA GAT TAC CCG TGG CTG AAC AAG TCG GCT TAT GTG Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr Val 710 715 720	2636
TTC GAT ATG TAC GGC TTC TAC AAA CCG GTG AAA AAC CTG ACT TTG CGT Phe Asp Met Tyr Gly Phe Tyr Lys Pro Val Lys Asn Leu Thr Leu Arg 725 730 735	2684
GCA GGC GTA TAT AAT GTG TTC AAC CGC AAA TAC ACC ACT TGG GAT TCC Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp Asp Ser 740 745 750	2732
CTG CGC GGC CTG TAT AGC TAC AGC ACC ACC AAC TCG GTC GAC CGC GAT Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ser Val Asp Arg Asp 755 760 765 770	2780
GGC AAA GGC TTA GAC CGC TAC CGC GCC CCA AGC CGT AAT TAC GCC GTA Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Ser Arg Asn Tyr Ala Val 775 780 785	2828
TCG CTG GAA TGG AAG TTT TA ATCTGGTATT ATTGAATTAA TCGCCTTGTT Ser Leu Glu Trp Lys Phe 790	2878
GAAAATTAAA GCCGTCCGAA TTGTGTTCAA GAACTCATTC GGACGGTTTT TACCGAATCT	2938
GTGTGTGGGT TTATAGTGGA TTAACAAAAA TCAGGACAAG GCGACGAAGC CGCAGACAGT	2998
ACAGATAGTA CGGAACCGAT TCACTTGGTG AGACCTTTGC AAAATTCCTT TCCCTCCCGA	3058
CAGCCGAAAC CCAAACACAG GTTTTCGGCT GTTTTCGCCC CAAATACCTC CTAATTCTAC	3118
CCAAATACCC CCTTAATCCT CCCCATAACC CGATAATCAG GCATCCGGCG CCTTTAGGCG	3178
GCAGCGGGCG CACTTAACCT GTTGGCGGCT TTCAAAGGT TCAAACACAT CGCCTTCAGG	3238
TGCCTTTGCG CACTCACTTT AATCAGTCCG AAATAGGCCG CCCGCGCATA GCAGAACTTA	3298

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cont.

CGGTGCAGCG TACCGAAGCT T

3319

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 792 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Pro Leu Gln Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
1 5 10 15
Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
20 25 30
Pro Val Lys Ala Glu Val Lys Ala Val Arg Gly Lys Gly Gln Arg Asn
35 40 45
Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu
50 55 60
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65 70 75 80
Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
85 90 95
Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp
100 105 110
Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
115 120 125
Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Asp Ile Val Lys
130 135 140
Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Gly Val
145 150 155 160
Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Pro Glu Arg Gln
165 170 175
Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp
180 185 190
Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
195 200 205
Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Lys
210 215 220
Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Asn Ile Arg Gly
225 230 235 240

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cont

Ser	Ala	Arg	Gly	Ile	Pro	Asp	Pro	Ser	Gln	His	Lys	Tyr	His	Ser	Phe
				245					250					255	
Leu	Gly	Lys	Ile	Ala	Tyr	Gln	Ile	Asn	Asp	Asn	His	Arg	Ile	Gly	Ala
			260					265					270		
Ser	Leu	Asn	Gly	Gln	Gln	Gly	His	Asn	Tyr	Thr	Val	Glu	Glu	Ser	Tyr
		275					280					285			
Asn	Leu	Leu	Ala	Ser	Tyr	Trp	Arg	Glu	Ala	Asp	Asp	Val	Asn	Arg	Arg
	290					295					300				
Arg	Asn	Thr	Asn	Leu	Phe	Tyr	Glu	Trp	Thr	Pro	Glu	Ser	Asp	Arg	Leu
305					310					315					320
Ser	Met	Val	Lys	Ala	Asp	Val	Asp	Tyr	Gln	Lys	Thr	Lys	Val	Ser	Ala
				325					330					335	
Val	Asn	Tyr	Lys	Gly	Ser	Phe	Pro	Ile	Glu	Asp	Ser	Ser	Thr	Leu	Thr
			340					345					350		
Arg	Asn	Tyr	Asn	Gln	Lys	Asp	Leu	Asp	Glu	Ile	Tyr	Asn	Arg	Ser	Met
		355					360					365			
Asp	Thr	Arg	Phe	Lys	Arg	Ile	Thr	Leu	Arg	Leu	Asp	Ser	His	Pro	Leu
	370					375					380				
Gln	Leu	Gly	Gly	Gly	Arg	His	Arg	Leu	Ser	Phe	Lys	Thr	Phe	Ala	Ser
385					390					395					400
Arg	Arg	Asp	Phe	Glu	Asn	Leu	Asn	Arg	Asp	Asp	Tyr	Tyr	Phe	Ser	Gly
			405						410					415	
Arg	Val	Val	Arg	Thr	Thr	Ser	Ser	Ile	Gln	His	Pro	Val	Lys	Thr	Thr
			420					425					430		
Asn	Tyr	Gly	Phe	Ser	Leu	Ser	Asp	Gln	Ile	Gln	Trp	Asn	Asp	Val	Phe
		435					440					445			
Ser	Ser	Arg	Ala	Gly	Ile	Arg	Tyr	Asp	His	Thr	Lys	Met	Thr	Pro	Gln
	450					455					460				
Glu	Leu	Asn	Ala	Glu	Cys	His	Ala	Cys	Asp	Lys	Thr	Pro	Pro	Ala	Ala
465					470					475					480
Asn	Thr	Tyr	Lys	Gly	Trp	Ser	Gly	Phe	Val	Gly	Leu	Ala	Ala	Gln	Leu
				485					490					495	
Asn	Gln	Ala	Trp	Arg	Val	Gly	Tyr	Asp	Ile	Thr	Ser	Gly	Tyr	Arg	Val
			500					505					510		
Pro	Asn	Ala	Ser	Glu	Val	Tyr	Phe	Thr	Tyr	Asn	His	Gly	Ser	Gly	Asn
		515					520					525			
Trp	Leu	Pro	Asn	Pro	Asn	Leu	Lys	Ala	Glu	Arg	Thr	Thr	Thr	His	Thr
	530					535					540				
Leu	Ser	Leu	Gln	Gly	Arg	Ser	Glu	Lys	Gly	Thr	Leu	Asp	Ala	Asn	Leu
545					550					555					560

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Cont.

Tyr Gln Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr
 565 570 575
 Thr Ser Gly Asp Val Ser Cys Thr Gln Met Asn Tyr Tyr Tyr Gly Met
 580 585 590
 Cys Ser Asn Pro Tyr Ser Glu Lys Leu Glu Trp Gln Met Gln Asn Ile
 595 600 605
 Asp Lys Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val
 610 615 620
 Asp Lys Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser
 625 630 635 640
 Leu Gly Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Phe
 645 650 655
 Thr Gln Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser
 660 665 670
 Glu Lys Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys
 675 680 685
 Val Lys Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr
 690 695 700
 Pro Leu Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala
 705 710 715 720
 Tyr Val Phe Asp Met Tyr Gly Phe Tyr Lys Pro Val Lys Asn Leu Thr
 725 730 735
 Leu Arg Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp
 740 745 750
 Asp Ser Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ser Val Asp
 755 760 765
 Arg Asp Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Ser Arg Asn Tyr
 770 775 780
 Ala Val Ser Leu Glu Trp Lys Phe
 785 790

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 Cont.

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG AAA CCA TTA CAA ATG CCC CCT ATC GCC GCG CTG CTC GGC AGT ATT	48
Met Lys Pro Leu Gln Met Pro Pro Ile Ala Ala Leu Leu Gly Ser Ile	
1 5 10 15	
TTC GGC AAT CCG GTC TTT GCG GCA GAT GAA GCT GCA ACT GAA ACC ACA	96
Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr	
20 25 30	
CCC GTT AAG GCA GAG GTA AAA GCA GTG CGC GTT AAA GGT CAG CGC AAT	144
Pro Val Lys Ala Glu Val Lys Ala Val Arg Val Lys Gly Gln Arg Asn	
35 40 45	
GCG CCT GCG GCT GTG GAA CGC GTC AAC CTT AAC CGT ATC AAA CAA GAA	192
Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu	
50 55 60	
ATG ATA CGC GAC AAT AAA GAC TTG GTG CGC TAT TCC ACC GAT GTC GGC	240
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly	
65 70 75 80	
TTG AGC GAC AGG AGC CGT CAT CAA AAA GGC TTT GCC ATT CGC GGC GTG	288
Leu Ser Asp Arg Ser Arg His Gln Lys Gly Phe Ala Ile Arg Gly Val	
85 90 95	
GAA GGC GAC CGT GTC GGC GTT AGT ATT GAC GGC GTA AAC CTG CCT GAT	336
Glu Gly Asp Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp	
100 105 110	
TCC GAA GAA AAC TCG CTG TAC GCC CGT TAT GGC AAC TTC AAC AGC TCG	384
Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser	
115 120 125	
CGT CTG TCT ATC GAC CCC GAA CTC GTG CGC AAC ATC GAC ATC GTA AAA	432
Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Asp Ile Val Lys	
130 135 140	
GGG GCG GAC TCT TTC AAT ACC GGC AGC GGC GCC TTG GGC GGC GGT GTG	480
Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Gly Val	
145 150 155 160	
AAT TAC CAA ACC CTG CAA GGA CGT GAC TTA CTG TTG CCT GAA CGG CAG	528
Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Pro Glu Arg Gln	
165 170 175	
TTC GGC GTG ATG ATG AAA AAC GGT TAC AGC ACG CGT AAC CGT GAA TGG	576
Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp	
180 185 190	
ACA AAT ACC CTC GGT TTC GGC GTG AGC AAC GAC CGC GTG GAT GCC GCT	624
Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala	
195 200 205	
TTG CTG TAT TCG CAA CGG CGC GGC CAT GAA ACT GAA AGC GCG GGC AAG	672
Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Lys	
210 215 220	

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Cont.

CGT GGT TAT CCG GTA GAG GGT GCT GGT AGC GGA GCG AAT ATC CGT GGT	720
Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Asn Ile Arg Gly	
225 230 235 240	
TCT GCG CGC GGT ATT CCT GAT CCG TCC CAA CAC AAA TAC CAC AGC TTC	768
Ser Ala Arg Gly Ile Pro Asp Pro Ser Gln His Lys Tyr His Ser Phe	
245 250 255	
TTG GGT AAG ATT GCT TAT CAA ATC AAC GAC AAC CAC CGC ATC GGC GCA	816
Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly Ala	
260 265 270	
TCG CTC AAC GGT CAG CAG GGG CAT AAT TAC ACG GTT GAA GAG TCT TAC	864
Ser Leu Asn Gly Gln Gln Gly His Asn Tyr Thr Val Glu Glu Ser Tyr	
275 280 285	
AAC CTG CTT GCT TCT TAT TGG CGT GAA GCT GAC GAT GTC AAC AGA CGG	912
Asn Leu Leu Ala Ser Tyr Trp Arg Glu Ala Asp Asp Val Asn Arg Arg	
290 295 300	
CGT AAC ACC AAC CTC TTT TAC GAA TGG ACG CCG GAA TCC GAC CGG TTG	960
Arg Asn Thr Asn Leu Phe Tyr Glu Trp Thr Pro Glu Ser Asp Arg Leu	
305 310 315 320	
TCT ATG GTA AAA GCG GAT GTC GAT TAT CAA AAA ACC AAA GTA TCT GCG	1008
Ser Met Val Lys Ala Asp Val Asp Tyr Gln Lys Thr Lys Val Ser Ala	
325 330 335	
GTC AAC TAC AAA GGT TCG TTC CCG ACG AAT TAC ACC ACA TGG GAA ACC	1056
Val Asn Tyr Lys Gly Ser Phe Pro Thr Asn Tyr Thr Thr Trp Glu Thr	
340 345 350	
GAG TAC CAT AAA AAG GAA GTT GGC GAA ATC TAT AAC CGC AGC ATG GAT	1104
Glu Tyr His Lys Lys Glu Val Gly Glu Ile Tyr Asn Arg Ser Met Asp	
355 360 365	
ACA ACC TTC AAA CGT ATT ACG CTG CGT ATG GAC AGC CAT CCG TTG CAA	1152
Thr Thr Phe Lys Arg Ile Thr Leu Arg Met Asp Ser His Pro Leu Gln	
370 375 380	
CTC GGG GGG GGG CGA CAC CGC CTG TCG TTT AAA ACC TTT GCC GGG CAG	1200
Leu Gly Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Ala Gly Gln	
385 390 395 400	
CGT GAT TTT GAA AAC TTA AAC CGC GAC GAT TAC TAC TTC AGC GGC CGT	1248
Arg Asp Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Gly Arg	
405 410 415	
GTT GTT CGA ACC ACC AAC AGT ATC CAG CAT CCG GTG AAA ACC ACC AAC	1296
Val Val Arg Thr Thr Asn Ser Ile Gln His Pro Val Lys Thr Thr Asn	
420 425 430	
TAC GGT TTC TCG CTG TCC GAC CAA ATC CAA TGG AAC GAC GTG TTC AGT	1344
Tyr Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser	
435 440 445	
AGC CGC GCA GGT ATC CGT TAC GAC CAC ACC AAA ATG ACG CCT CAG GAA	1392
Ser Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu	

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cont

450	455	460	
TTG AAT GCC GAC TGT CAT GCT TGT GAC AAA ACA CCG CCT GCA GCC AAC			1440
Leu Asn Ala Asp Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn			
465	470	475	480
ACT TAT AAA GGC TGG AGC GGA TTT GTC GGC TTG GCG GCG CAG CTG AGC			1488
Thr Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Ser			
	485	490	495
CAA ACA TGG CGT TTG GGT TAC GAT GTG ACC TCA GGT TTC CGC GTG CCG			1536
Gln Thr Trp Arg Leu Gly Tyr Asp Val Thr Ser Gly Phe Arg Val Pro			
	500	505	510
AAT GCG TCT GAA GTG TAT TTC ACT TAC AAC CAC GGT TCG GGC ACT TGG			1584
Asn Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Thr Trp			
	515	520	525
AAG CCT AAT CCT AAT TTG AAG GCA GAA CGC AGC ACC ACC CAC ACC CTG			1632
Lys Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu			
	530	535	540
TCC TTG CAG GGG CGC GGC GAC AAA GGG ACA CTG GAT GCC AAC CTG TAT			1680
Ser Leu Gln Gly Arg Gly Asp Lys Gly Thr Leu Asp Ala Asn Leu Tyr			
	545	550	555
CAA AGC AAT TAC CGA AAC TTC CTG TCG GAA GAG CAG AAT CTG ACT GTC			1728
Gln Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Asn Leu Thr Val			
	565	570	575
AGC GGC ACA CCC GGC TGT ACT GAG GAG GAT GCT TAC TAC TAT AGA TGC			1776
Ser Gly Thr Pro Gly Cys Thr Glu Glu Asp Ala Tyr Tyr Tyr Arg Cys			
	580	585	590
AGC GAC CCC TAC AAA GAA AAA CTG GAT TGG CAG ATG AAA AAT ATC GAC			1824
Ser Asp Pro Tyr Lys Glu Lys Leu Asp Trp Gln Met Lys Asn Ile Asp			
	595	600	605
AAG GCC AGA ATC CGC GGT ATC GAG TTG ACA GGC CGT CTG AAT GTG GAC			1872
Lys Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val Asp			
	610	615	620
AAA GTA GCG TCT TTT GTT CCT GAG GGT TGG AAA CTG TTC GGC TCG CTG			1920
Lys Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu			
	625	630	635
GGT TAT GCG AAA AGC AAA CTG TCG GGC GAC AAC AGC CTG CTG TCC ACA			1968
Gly Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr			
	645	650	655
CAG CCG CTG AAA GTG ATT GCC GGT ATC GAC TAT GAA AGT CCG AGC GAA			2016
Gln Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu			
	660	665	670
AAA TGG GGC GTA TTC TCC CGC CTG ACC TAT CTA GGC GCG AAA AAG GTC			2064
Lys Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val			
	675	680	685

B1
Cont

AAA GAC GCG CAA TAC ACC GTT TAT GAA AAC AAG GGC TGG GGT ACG CCT	2112
Lys Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr Pro	
690 695 700	
TTG CAG AAA AAG GTA AAA GAT TAC CCG TGG CTG AAC AAG TCG GCT TAT	2160
Leu Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr	
705 710 715 720	
GTG TTT GAT ATG TAC GGC TTC TAC AAA CCG GCT AAA AAC CTG ACT TTG	2208
Val Phe Asp Met Tyr Gly Phe Tyr Lys Pro Ala Lys Asn Leu Thr Leu	
725 730 735	
CGT GCA GGC GTG TAC AAC CTG TTC AAC CGC AAA TAC ACC ACT TGG GAT	2256
Arg Ala Gly Val Tyr Asn Leu Phe Asn Arg Lys Tyr Thr Thr Trp Asp	
740 745 750	
TCC CTG CGC GGT TTA TAT AGC TAC AGC ACC ACC AAT GCG GTC GAC CGC	2304
Ser Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ala Val Asp Arg	
755 760 765	
GAT GGC AAA GGC TTA GAC CGC TAC CGC GCC CCA GGC CGC AAT TAC GCC	2352
Asp Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Gly Arg Asn Tyr Ala	
770 775 780	
GTA TCG CTG GAA TGG AAG TTT TAA	2376
Val Ser Leu Glu Trp Lys Phe	
785 790	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

B1 Cons

Met Lys Pro Leu Gln Met Pro Pro Ile Ala Ala Leu Leu Gly Ser Ile	
1 5 10 15	
Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr	
20 25 30	
Pro Val Lys Ala Glu Val Lys Ala Val Arg Val Lys Gly Gln Arg Asn	
35 40 45	
Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu	
50 55 60	
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly	
65 70 75 80	
Leu Ser Asp Arg Ser Arg His Gln Lys Gly Phe Ala Ile Arg Gly Val	

85					90					95					
Glu	Gly	Asp	Arg	Val	Gly	Val	Ser	Ile	Asp	Gly	Val	Asn	Leu	Pro	Asp
			100					105					110		
Ser	Glu	Glu	Asn	Ser	Leu	Tyr	Ala	Arg	Tyr	Gly	Asn	Phe	Asn	Ser	Ser
		115					120					125			
Arg	Leu	Ser	Ile	Asp	Pro	Glu	Leu	Val	Arg	Asn	Ile	Asp	Ile	Val	Lys
	130					135					140				
Gly	Ala	Asp	Ser	Phe	Asn	Thr	Gly	Ser	Gly	Ala	Leu	Gly	Gly	Gly	Val
145						150					155				160
Asn	Tyr	Gln	Thr	Leu	Gln	Gly	Arg	Asp	Leu	Leu	Leu	Pro	Glu	Arg	Gln
				165					170					175	
Phe	Gly	Val	Met	Met	Lys	Asn	Gly	Tyr	Ser	Thr	Arg	Asn	Arg	Glu	Trp
			180					185					190		
Thr	Asn	Thr	Leu	Gly	Phe	Gly	Val	Ser	Asn	Asp	Arg	Val	Asp	Ala	Ala
			195				200					205			
Leu	Leu	Tyr	Ser	Gln	Arg	Arg	Gly	His	Glu	Thr	Glu	Ser	Ala	Gly	Lys
	210					215					220				
Arg	Gly	Tyr	Pro	Val	Glu	Gly	Ala	Gly	Ser	Gly	Ala	Asn	Ile	Arg	Gly
225						230					235				240
Ser	Ala	Arg	Gly	Ile	Pro	Asp	Pro	Ser	Gln	His	Lys	Tyr	His	Ser	Phe
				245					250					255	
Leu	Gly	Lys	Ile	Ala	Tyr	Gln	Ile	Asn	Asp	Asn	His	Arg	Ile	Gly	Ala
			260					265					270		
Ser	Leu	Asn	Gly	Gln	Gln	Gly	His	Asn	Tyr	Thr	Val	Glu	Glu	Ser	Tyr
		275					280					285			
Asn	Leu	Leu	Ala	Ser	Tyr	Trp	Arg	Glu	Ala	Asp	Asp	Val	Asn	Arg	Arg
	290					295					300				
Arg	Asn	Thr	Asn	Leu	Phe	Tyr	Glu	Trp	Thr	Pro	Glu	Ser	Asp	Arg	Leu
305						310					315				320
Ser	Met	Val	Lys	Ala	Asp	Val	Asp	Tyr	Gln	Lys	Thr	Lys	Val	Ser	Ala
				325					330					335	
Val	Asn	Tyr	Lys	Gly	Ser	Phe	Pro	Thr	Asn	Tyr	Thr	Thr	Trp	Glu	Thr
			340					345					350		
Glu	Tyr	His	Lys	Lys	Glu	Val	Gly	Glu	Ile	Tyr	Asn	Arg	Ser	Met	Asp
		355					360					365			
Thr	Thr	Phe	Lys	Arg	Ile	Thr	Leu	Arg	Met	Asp	Ser	His	Pro	Leu	Gln
	370					375					380				
Leu	Gly	Gly	Gly	Arg	His	Arg	Leu	Ser	Phe	Lys	Thr	Phe	Ala	Gly	Gln
385						390					395				400

B1
cont.

Arg	Asp	Phe	Glu	Asn	Leu	Asn	Arg	Asp	Asp	Tyr	Tyr	Phe	Ser	Gly	Arg	405	410	415
Val	Val	Arg	Thr	Thr	Asn	Ser	Ile	Gln	His	Pro	Val	Lys	Thr	Thr	Asn	420	425	430
Tyr	Gly	Phe	Ser	Leu	Ser	Asp	Gln	Ile	Gln	Trp	Asn	Asp	Val	Phe	Ser	435	440	445
Ser	Arg	Ala	Gly	Ile	Arg	Tyr	Asp	His	Thr	Lys	Met	Thr	Pro	Gln	Glu	450	455	460
Leu	Asn	Ala	Asp	Cys	His	Ala	Cys	Asp	Lys	Thr	Pro	Pro	Ala	Ala	Asn	465	470	475
Thr	Tyr	Lys	Gly	Trp	Ser	Gly	Phe	Val	Gly	Leu	Ala	Ala	Gln	Leu	Ser	485	490	495
Gln	Thr	Trp	Arg	Leu	Gly	Tyr	Asp	Val	Thr	Ser	Gly	Phe	Arg	Val	Pro	500	505	510
Asn	Ala	Ser	Glu	Val	Tyr	Phe	Thr	Tyr	Asn	His	Gly	Ser	Gly	Thr	Trp	515	520	525
Lys	Pro	Asn	Pro	Asn	Leu	Lys	Ala	Glu	Arg	Ser	Thr	Thr	His	Thr	Leu	530	535	540
Ser	Leu	Gln	Gly	Arg	Gly	Asp	Lys	Gly	Thr	Leu	Asp	Ala	Asn	Leu	Tyr	545	550	555
Gln	Ser	Asn	Tyr	Arg	Asn	Phe	Leu	Ser	Glu	Glu	Gln	Asn	Leu	Thr	Val	565	570	575
Ser	Gly	Thr	Pro	Gly	Cys	Thr	Glu	Glu	Asp	Ala	Tyr	Tyr	Tyr	Arg	Cys	580	585	590
Ser	Asp	Pro	Tyr	Lys	Glu	Lys	Leu	Asp	Trp	Gln	Met	Lys	Asn	Ile	Asp	595	600	605
Lys	Ala	Arg	Ile	Arg	Gly	Ile	Glu	Leu	Thr	Gly	Arg	Leu	Asn	Val	Asp	610	615	620
Lys	Val	Ala	Ser	Phe	Val	Pro	Glu	Gly	Trp	Lys	Leu	Phe	Gly	Ser	Leu	625	630	635
Gly	Tyr	Ala	Lys	Ser	Lys	Leu	Ser	Gly	Asp	Asn	Ser	Leu	Leu	Ser	Thr	645	650	655
Gln	Pro	Leu	Lys	Val	Ile	Ala	Gly	Ile	Asp	Tyr	Glu	Ser	Pro	Ser	Glu	660	665	670
Lys	Trp	Gly	Val	Phe	Ser	Arg	Leu	Thr	Tyr	Leu	Gly	Ala	Lys	Lys	Val	675	680	685
Lys	Asp	Ala	Gln	Tyr	Thr	Val	Tyr	Glu	Asn	Lys	Gly	Trp	Gly	Thr	Pro	690	695	700
Leu	Gln	Lys	Lys	Val	Lys	Asp	Tyr	Pro	Trp	Leu	Asn	Lys	Ser	Ala	Tyr	705	710	715
																		720

B1
cont.

Val Phe Asp Met Tyr Gly Phe Tyr Lys Pro Ala Lys Asn Leu Thr Leu
725 730 735

Arg Ala Gly Val Tyr Asn Leu Phe Asn Arg Lys Tyr Thr Thr Trp Asp
740 745 750

Ser Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ala Val Asp Arg
755 760 765

Asp Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Gly Arg Asn Tyr Ala
770 775 780

Val Ser Leu Glu Trp Lys Phe
785 790

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..2376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG AAA CCA TTA CAA ATG CTC CCT ATC GCC GCG CTG GTC GGC AGT ATT 48
Met Lys Pro Leu Gln Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
1 5 10 15

TTC GGC AAT CCG GTC TTT GCG GCA GAT GAA GCT GCA ACT GAA ACC ACA 96
Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
20 25 30

CCC GTT AAG GCA GAG GTA AAA GCA GTG CGC GTT AAA GGC CAG CGC AAT 144
Pro Val Lys Ala Glu Val Lys Ala Val Arg Val Lys Gly Gln Arg Asn
35 40 45

GCG CCT GCG GCT GTG GAA CGC GTC AAC CTT AAC CGT ATC AAA CAA GAA 192
Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu
50 55 60

ATG ATA CGC GAC AAC AAA GAC TTG GTG CGC TAT TCC ACC GAT GTC GGC 240
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65 70 75 80

TTG AGC GAC AGC GGC CGC CAT CAA AAA GGC TTT GCC GTT CGC GGC GTG 288
Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
85 90 95

GAA GGC AAC CGT GTC GGC GTG AGC ATA GAC GGC GTA AAC CTG CCT GAT 336
Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp
100 105 110

B1
Cont.

TCC	GAA	GAA	AAC	TCG	CTG	TAC	GCC	CGT	TAT	GGC	AAC	TTC	AAC	AGC	TCG	384
Ser	Glu	Glu	Asn	Ser	Leu	Tyr	Ala	Arg	Tyr	Gly	Asn	Phe	Asn	Ser	Ser	
		115					120					125				
CGT	CTG	TCT	ATC	GAC	CCC	GAA	CTC	GTG	CGC	AAC	ATC	GAG	ATC	GTA	AAA	432
Arg	Leu	Ser	Ile	Asp	Pro	Glu	Leu	Val	Arg	Asn	Ile	Glu	Ile	Val	Lys	
	130					135					140					
GGG	GCG	GAC	TCT	TTC	AAT	ACC	GGC	AGC	GGC	GCC	TTG	GGC	GGC	GGT	GTG	480
Gly	Ala	Asp	Ser	Phe	Asn	Thr	Gly	Ser	Gly	Ala	Leu	Gly	Gly	Gly	Val	
145					150					155					160	
AAT	TAC	CAA	ACC	CTG	CAA	GGA	CGT	GAC	TTA	CTG	TTG	GAT	GAC	CGG	CAG	528
Asn	Tyr	Gln	Thr	Leu	Gln	Gly	Arg	Asp	Leu	Leu	Leu	Asp	Asp	Arg	Gln	
				165					170					175		
TTC	GGC	GTG	ATG	ATG	AAA	AAC	GGT	TAC	AGC	ACG	CGT	AAC	CGT	GAA	TGG	576
Phe	Gly	Val	Met	Met	Lys	Asn	Gly	Tyr	Ser	Thr	Arg	Asn	Arg	Glu	Trp	
			180					185					190			
ACA	AAT	ACC	CTC	GGT	TTC	GGC	GTG	AGC	AAC	GAC	CGC	GTG	GAT	GCC	GCT	624
Thr	Asn	Thr	Leu	Gly	Phe	Gly	Val	Ser	Asn	Asp	Arg	Val	Asp	Ala	Ala	
		195					200					205				
TTG	CTG	TAT	TCG	CAA	CGG	CGC	GGC	CAT	GAA	ACT	GAA	AGC	GCG	GGC	AAC	672
Leu	Leu	Tyr	Ser	Gln	Arg	Arg	Gly	His	Glu	Thr	Glu	Ser	Ala	Gly	Asn	
	210					215					220					
CGT	GGT	TAT	CCG	GTA	GAG	GGT	GCT	GGT	AAA	GAA	ACT	AAT	ATC	CGT	GGT	720
Arg	Gly	Tyr	Pro	Val	Glu	Gly	Ala	Gly	Lys	Glu	Thr	Asn	Ile	Arg	Gly	
225					230				235						240	
TCT	GCG	CGC	GGT	ATT	CCT	GAT	CCG	TCC	AAA	CAC	AAA	TAC	CAC	AAC	TTC	768
Ser	Ala	Arg	Gly	Ile	Pro	Asp	Pro	Ser	Lys	His	Lys	Tyr	His	Asn	Phe	
				245					250					255		
TTG	GGT	AAG	ATT	GCT	TAT	CAA	ATC	AAC	GAC	AAC	CAC	CGC	ATC	GGC	GCA	816
Leu	Gly	Lys	Ile	Ala	Tyr	Gln	Ile	Asn	Asp	Asn	His	Arg	Ile	Gly	Ala	
			260					265					270			
TCG	CTC	AAC	GGT	CAG	CAG	GGG	CAT	AAT	TAC	ACG	GTT	GAA	GAG	TCT	TAC	864
Ser	Leu	Asn	Gly	Gln	Gln	Gly	His	Asn	Tyr	Thr	Val	Glu	Glu	Ser	Tyr	
		275					280					285				
AAC	CTG	ACT	GCT	TCT	TCT	TGG	CGT	GAA	GCT	GAC	GAT	GTC	AAC	AGA	CGG	912
Asn	Leu	Thr	Ala	Ser	Ser	Trp	Arg	Glu	Ala	Asp	Asp	Val	Asn	Arg	Arg	
	290					295					300					
CGT	AAC	GCT	AAC	CTC	TTT	TAC	GAA	TGG	ATG	CCG	GAT	TCC	AAC	TGG	TTG	960
Arg	Asn	Ala	Asn	Leu	Phe	Tyr	Glu	Trp	Met	Pro	Asp	Ser	Asn	Trp	Leu	
305				310					315						320	
TCT	TCT	CTC	AAA	GCG	GAT	TTC	GAT	TAT	CAA	AAA	ACC	AAA	GTA	GCT	GCG	1008
Ser	Ser	Leu	Lys	Ala	Asp	Phe	Asp	Tyr	Gln	Lys	Thr	Lys	Val	Ala	Ala	
				325					330					335		
ATC	AAC	AAA	GGT	TCG	TTC	CCG	ACT	AAC	TAT	ACC	ACC	TGG	GAA	ACC	GAA	1056
Ile	Asn	Lys	Gly	Ser	Phe	Pro	Thr	Asn	Tyr	Thr	Thr	Trp	Glu	Thr	Glu	

B1
Cont.

340	345	350	
TAC CAT CAA AAG GAA GTT GGT GAA ATC TAC AAC CGC AGT ATG GAT ACC Tyr His Lys Lys Glu Val Gly Glu Ile Tyr Asn Arg Ser Met Asp Thr 355 360 365			1104
CGC TTC AAA CGT TTT ACG CTG CGT TTG GAC AGC CAT CCG TTG CAA CTC Arg Phe Lys Arg Phe Thr Leu Arg Leu Asp Ser His Pro Leu Gln Leu 370 375 380			1152
GGG GGG GGG CGA CAC CGC CTG TCG TTT AAA ACT TTC GCC AGC CGC CGT Gly Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Ala Ser Arg Arg 385 390 395 400			1200
GAT TTT GAA AAC CTA AAC CGC GAC TAT TAC TAC TTC AGC GGC CGT GTT Asp Phe Glu Asn Leu Asn Arg Asp Tyr Tyr Tyr Phe Ser Gly Arg Val 405 410 415			1248
GTT CGA ACC ACC AGC AGT ATC CAG CAT CCG GTG AAA ACC ACC AAC TAC Val Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr Asn Tyr 420 425 430			1296
GGT TTC TCA CTG TCT GAC CAA ATT CAA TGG AAC GAC GTG TTC AGT AGC Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser Ser 435 440 445			1344
CGC GCA GGT ATC CGT TAC GAT CAT ACC AAA ATG ACG CCT CAG GAA TTG Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu Leu 450 455 460			1392
AAT GCC GAG TGT CAT GCT TGT GAC AAA ACA CCG CCT GCA GCC AAC ACT Asn Ala Glu Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn Thr 465 470 475 480			1440
TAT AAA GGC TGG AGC GGT TTT GTC GGC TTG GCG GCG CAA CTG AAT CAG Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Asn Gln 485 490 495			1488
GCT TGG CGT GTC GGT TAC GAC ATT ACT TCC GGC TAC CGT GTC CCC AAT Ala Trp Arg Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val Pro Asn 500 505 510			1536
GCG TCC GAA GTG TAT TTC ACT TAC AAC CAC GGT TCG GGT AAT TGG CTG Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn Trp Leu 515 520 525			1584
CCC AAT CCC AAC CTG AAA GCC GAG CGC TCG ACC ACC CAC ACC CTC TCT Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu Ser 530 535 540			1632
CTG CAA GGC CGC AGC GAA AAA GGT ACT TTG GAT GCC AAC CTG TAT CAA Leu Gln Gly Arg Ser Glu Lys Gly Thr Leu Asp Ala Asn Leu Tyr Gln 545 550 555 560			1680
AGC AAT TAC CGA AAT TTC CTG TCT GAA GAG CAG AAG CTG ACC ACC AGC Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr Thr Ser 565 570 575			1728

B1
cont

GGC ACT CCC GGC TGT ACT GAG GAG AAT GCC TAC TAC TCT ATC TGT AGC Gly Thr Pro Gly Cys Thr Glu Glu Asn Ala Tyr Tyr Ser Ile Cys Ser 580 585 590	1776
GAC CCT TAT AAG GAA AAA CTG GAA TGG CAG ATG CAA AAT ATC GAC AAG Asp Pro Tyr Lys Glu Lys Leu Glu Trp Gln Met Gln Asn Ile Asp Lys 595 600 605	1824
GCC AGA ATC CGC GGT ATC GAG CTG ACG GGC CGT CTG AAT GTG GAC AAA Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val Asp Lys 610 615 620	1872
GTA GCG TCT TTT GTT CCT GAG GGC TGG AAA CTG TTC GGC TCG CTG GGT Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu Gly 625 630 635 640	1920
TAT GCG AAA AGC AAA CTG TCG GGC GAC AAC AGC CTG CTG TCC ACC CAG Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr Gln 645 650 655	1968
CCG TTG AAA GTG ATT GCC GGT ATC GAC TAT GAA AGT CCG AGC GAA AAA Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu Lys 660 665 670	2016
TGG GGC GTG TTC TCC CGC CTG ACC TAT CTG GGC GCG AAA AAG GTC AAA Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val Lys 675 680 685	2064
GAC GCG CAA TAC ACC GTT TAT GAA AAC AAG GGC TGG GGT ACG CCT TTG Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr Pro Leu 690 695 700	2112
CAG AAA AAG GTA AAA GAT TAC CCG TGG CTG AAC AAG TCG GCT TAT GTG Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr Val 705 710 715 720	2160
TTC GAT ATG TAC GGC TTC TAC AAA CCG GTG AAA AAC CTG ACT TTG CGT Phe Asp Met Tyr Gly Phe Tyr Lys Pro Val Lys Asn Leu Thr Leu Arg 725 730 735	2208
GCA GGC GTA TAT AAT GTG TTC AAC CGC AAA TAC ACC ACT TGG GAT TCC Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp Asp Ser 740 745 750	2256
CTG CGC GGC CTG TAT AGC TAC AGC ACC ACC AAC TCG GTC GAC CGC GAT Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ser Val Asp Arg Asp 755 760 765	2304
GGC AAA GGC TTA GAC CGC TAC CGC GCC CCA GGC CGT AAT TAC GCC GTA Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Gly Arg Asn Tyr Ala Val 770 775 780	2352
TCG CTG GAA TGG AAG TTT TAA Ser Leu Glu Trp Lys Phe 785 790	2379

B1
Cont.

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Lys Pro Leu Gln Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
1 5 10 15
Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
20 25 30
Pro Val Lys Ala Glu Val Lys Ala Val Arg Val Lys Gly Gln Arg Asn
35 40 45
Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu
50 55 60
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65 70 75 80
Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
85 90 95
Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp
100 105 110
Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
115 120 125
Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Glu Ile Val Lys
130 135 140
Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Gly Val
145 150 155 160
Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Asp Asp Arg Gln
165 170 175
Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp
180 185 190
Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
195 200 205
Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Asn
210 215 220
Arg Gly Tyr Pro Val Glu Gly Ala Gly Lys Glu Thr Asn Ile Arg Gly
225 230 235 240
Ser Ala Arg Gly Ile Pro Asp Pro Ser Lys His Lys Tyr His Asn Phe
245 250 255

31
cont

Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly Ala
 260 265 270
 Ser Leu Asn Gly Gln Gln Gly His Asn Tyr Thr Val Glu Glu Ser Tyr
 275 280 285
 Asn Leu Thr Ala Ser Ser Trp Arg Glu Ala Asp Asp Val Asn Arg Arg
 290 295 300
 Arg Asn Ala Asn Leu Phe Tyr Glu Trp Met Pro Asp Ser Asn Trp Leu
 305 310 315 320
 Ser Ser Leu Lys Ala Asp Phe Asp Tyr Gln Lys Thr Lys Val Ala Ala
 325 330 335
 Ile Asn Lys Gly Ser Phe Pro Thr Asn Tyr Thr Thr Trp Glu Thr Glu
 340 345 350
 Tyr His Lys Lys Glu Val Gly Glu Ile Tyr Asn Arg Ser Met Asp Thr
 355 360 365
 Arg Phe Lys Arg Phe Thr Leu Arg Leu Asp Ser His Pro Leu Gln Leu
 370 375 380
 Gly Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Ala Ser Arg Arg
 385 390 395 400
 Asp Phe Glu Asn Leu Asn Arg Asp Tyr Tyr Tyr Phe Ser Gly Arg Val
 405 410 415
 Val Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr Asn Tyr
 420 425 430
 Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser Ser
 435 440 445
 Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu Leu
 450 455 460
 Asn Ala Glu Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn Gln
 465 470 475 480
 Asn Thr Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu
 485 490 495
 Ala Trp Arg Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val Pro Asn
 500 505 510
 Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn Trp Leu
 515 520 525
 Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu Ser
 530 535 540
 Leu Gln Gly Arg Ser Glu Lys Gly Met Leu Asp Ala Asn Leu Tyr Gln
 545 550 555 560
 Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr Thr Ser
 565 570 575

B!
 cont.

Gly	Thr	Pro	Gly	Cys	Thr	Glu	Glu	Asn	Ala	Tyr	Tyr	Ser	Ile	Cys	Ser	580	585	590	
Asp	Pro	Tyr	Lys	Glu	Lys	Leu	Glu	Trp	Gln	Met	Lys	Asn	Ile	Asp	Lys	595	600	605	
Ala	Arg	Ile	Arg	Gly	Ile	Glu	Leu	Thr	Gly	Arg	Leu	Asn	Val	Asp	Lys	610	615	620	
Val	Ala	Ser	Phe	Val	Pro	Glu	Gly	Trp	Lys	Leu	Phe	Gly	Ser	Leu	Gly	625	630	635	640
Tyr	Ala	Lys	Ser	Lys	Leu	Ser	Gly	Asp	Asn	Ser	Leu	Leu	Ser	Thr	Gln	645	650	655	
Pro	Leu	Lys	Val	Ile	Ala	Gly	Ile	Asp	Tyr	Glu	Ser	Pro	Ser	Glu	Lys	660	665	670	
Trp	Gly	Val	Phe	Ser	Arg	Leu	Thr	Tyr	Leu	Gly	Ala	Lys	Lys	Val	Lys	675	680	685	
Asp	Ala	Gln	Tyr	Thr	Val	Tyr	Glu	Asn	Lys	Gly	Trp	Gly	Thr	Pro	Leu	690	695	700	
Gln	Lys	Lys	Val	Lys	Asp	Tyr	Pro	Trp	Leu	Asn	Lys	Ser	Ala	Tyr	Val	705	710	715	720
Phe	Asp	Met	Tyr	Gly	Phe	Tyr	Lys	Pro	Val	Lys	Asn	Leu	Thr	Leu	Arg	725	730	735	
Ala	Gly	Val	Tyr	Asn	Leu	Phe	Asn	Arg	Lys	Tyr	Thr	Thr	Trp	Asp	Ser	740	745	750	
Leu	Arg	Gly	Leu	Tyr	Ser	Tyr	Ser	Thr	Thr	Asn	Ala	Val	Asp	Arg	Asp	755	760	765	
Gly	Lys	Gly	Leu	Asp	Arg	Tyr	Arg	Ala	Pro	Gly	Arg	Asn	Tyr	Ala	Val	770	775	780	
Ser	Leu	Glu	Trp	Lys	Phe											785	790		

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

B1
Cont.

ATG	AAA	CCA	TTA	CAC	ATG	CTT	CCT	ATT	GCC	GCG	CTG	GTC	GGC	AGT	ATT	48
Met	Lys	Pro	Leu	His	Met	Leu	Pro	Ile	Ala	Ala	Leu	Val	Gly	Ser	Ile	
1				5					10					15		
TTC	GGC	AAT	CCG	GTC	TTG	GCA	GCG	GAT	GAA	GCT	GCA	ACC	GAA	ACC	ACA	96
Phe	Gly	Asn	Pro	Val	Leu	Ala	Ala	Asp	Glu	Ala	Ala	Thr	Glu	Thr	Thr	
			20					25					30			
CCC	GTT	AAA	GCA	GAG	ATA	AAA	GAA	GTG	CGC	GTT	AAA	GAC	CAG	CTT	AAT	144
Pro	Val	Lys	Ala	Glu	Ile	Lys	Glu	Val	Arg	Val	Lys	Asp	Gln	Leu	Asn	
		35					40					45				
GCG	CCT	GCA	ACC	GTG	GAA	CGT	GTC	AAC	CTC	GGC	CGC	ATT	CAA	CAG	GAA	192
Ala	Pro	Ala	Thr	Val	Glu	Arg	Val	Asn	Leu	Gly	Arg	Ile	Gln	Gln	Glu	
	50					55					60					
ATG	ATA	CGC	GAC	AAC	AAA	GAC	TTG	GTG	CGT	TAC	TCC	ACC	GAC	GTC	GGC	240
Met	Ile	Arg	Asp	Asn	Lys	Asp	Leu	Val	Arg	Tyr	Ser	Thr	Asp	Val	Gly	
65					70				75					80		
TTG	AGC	GAT	AGC	GGC	CGC	CAT	CAA	AAA	GGC	TTT	GCT	GTG	CGC	GGC	GTG	288
Leu	Ser	Asp	Ser	Gly	Arg	His	Gln	Lys	Gly	Phe	Ala	Val	Arg	Gly	Val	
				85					90					95		
GAA	GGC	AAC	CGT	GTC	GGT	GTC	AGC	ATT	GAC	GGC	GTG	AGC	CTG	CCT	GAT	336
Glu	Gly	Asn	Arg	Val	Gly	Val	Ser	Ile	Asp	Gly	Val	Ser	Leu	Pro	Asp	
		100						105					110			
TCG	GAA	GAA	AAC	TCA	CTG	TAT	GCA	CGT	TAT	GGC	AAC	TTC	AAC	AGC	TCG	384
Ser	Glu	Glu	Asn	Ser	Leu	Tyr	Ala	Arg	Tyr	Gly	Asn	Phe	Asn	Ser	Ser	
	115						120					125				
CGC	CTG	TCT	ATC	GAC	CCC	GAA	CTC	GTG	CGC	AAC	ATC	GAA	ATC	GCG	AAG	432
Arg	Leu	Ser	Ile	Asp	Pro	Glu	Leu	Val	Arg	Asn	Ile	Glu	Ile	Ala	Lys	
	130					135					140					
GGC	GCT	GAC	TCT	TTC	AAT	ACC	GGT	AGC	GGC	GCA	TTG	GGT	GGC	GGC	GTG	480
Gly	Ala	Asp	Ser	Phe	Asn	Thr	Gly	Ser	Gly	Ala	Leu	Gly	Gly	Gly	Val	
145					150				155						160	
AAT	TAC	CAA	ACC	CTG	CAA	GGA	CAT	GAT	TTG	CTG	TTG	GAC	GAC	AGG	CAA	528
Asn	Tyr	Gln	Thr	Leu	Gln	Gly	His	Asp	Leu	Leu	Leu	Asp	Asp	Arg	Gln	
				165					170					175		
TTC	GGC	GTG	ATG	ATG	AAA	AAC	GGT	TAC	AGC	ACG	CGC	AAC	CGC	GAA	TGG	576
Phe	Gly	Val	Met	Met	Lys	Asn	Gly	Tyr	Ser	Thr	Arg	Asn	Arg	Glu	Trp	
			180					185					190			
ACA	AAT	ACA	CTC	GGT	TTC	GGT	GTG	AGC	AAC	GAC	CGC	GTG	GAT	GCC	GCT	624
Thr	Asn	Thr	Leu	Gly	Phe	Gly	Val	Ser	Asn	Asp	Arg	Val	Asp	Ala	Ala	
		195					200					205				
TTG	CTG	TAT	TCG	CAA	CGT	CGC	GGT	CAT	GAG	ACC	GAA	AGC	GCG	GGC	GAG	672
Leu	Leu	Tyr	Ser	Gln	Arg	Arg	Gly	His	Glu	Thr		Ser	Ala	Gly	Glu	
	210					215					220					
CGT	GGC	TAT	CCG	GTA	GAG	GGT	GCT	GGC	AGC	GGA	GCA	ATT	ATC	CGT	GGT	720
Arg	Gly	Tyr	Pro	Val	Glu	Gly	Ala	Gly	Ser	Gly	Ala	Ile	Ile	Arg	Gly	
225					230					235					240	

B1
Cont

TCG	TCA	CGC	GGT	ATC	CCT	GAT	CCG	TCC	AAA	CAC	AAA	TAC	CAC	AAC	TTC	768
Ser	Ser	Arg	Gly	Ile	Pro	Asp	Pro	Ser	Lys	His	Lys	Tyr	His	Asn	Phe	
			245						250					255		
TTG	GGT	AAG	ATT	GCT	TAT	CAA	ATC	AAC	GAC	AAG	CAC	CGC	ATC	GGC	CCA	816
Leu	Gly	Lys	Ile	Ala	Tyr	Gln	Ile	Asn	Asp	Lys	His	Arg	Ile	Gly	Pro	
			260					265					270			
TCG	TTT	AAC	GGC	CAG	CAG	GGG	CAT	AAT	TAC	ACG	ATT	GAA	GAG	TCT	TAT	864
Ser	Phe	Asn	Gly	Gln	Gln	Gly	His	Asn	Tyr	Thr	Ile	Glu	Glu	Ser	Tyr	
		275					280					285				
AAC	CTG	ACC	GCT	TCT	TCC	TGG	CGC	GAA	GCC	GAT	GAC	GTA	AAC	AGA	CGG	912
Asn	Leu	Thr	Ala	Ser	Ser	Trp	Arg	Glu	Ala	Asp	Asp	Val	Asn	Arg	Arg	
	290					295					300					
CGC	AAT	GCC	AAC	CTC	TTT	TAC	GAA	TGG	ACG	CCT	GAT	TCA	AAT	TGG	CTG	960
Arg	Asn	Ala	Asn	Leu	Phe	Tyr	Glu	Trp	Thr	Pro	Asp	Ser	Asn	Trp	Leu	
305				310						315					320	
TCG	TCT	TTG	AAG	GCG	GAT	TTC	GAT	TAT	CAG	ACA	ACC	AAA	GTG	GCG	GCG	1008
Ser	Ser	Leu	Lys	Ala	Asp	Phe	Asp	Tyr	Gln	Thr	Thr	Lys	Val	Ala	Ala	
			325						330					335		
GTT	AAC	AAC	AAA	GGC	TCG	TTC	CCG	ACG	GAT	TAT	TCC	ACC	TTG	ACG	CGC	1056
Val	Asn	Asn	Lys	Gly	Ser	Phe	Pro	Thr	Asp	Tyr	Ser	Thr	Leu	Thr	Arg	
			340					345					350			
AAC	TAT	AAT	CAG	AAG	GAT	TTG	GAG	AAT	ATA	TAC	AAC	CGC	AGC	ATG	GAC	1104
Asn	Tyr	Asn	Gln	Lys	Asp	Leu	Glu	Asn	Ile	Tyr	Asn	Arg	Ser	Met	Asp	
		355					360					365				
ACC	CGA	TTC	AAA	CGT	TTT	ACT	TTG	CGT	ATG	GAC	AGC	CAA	CCG	TTG	CAA	1152
Thr	Arg	Phe	Lys	Arg	Phe	Thr	Leu	Arg	Met	Asp	Ser	Gln	Pro	Leu	Gln	
	370					375					380					
CTG	GGC	GGC	CAA	CAT	CGC	TTG	TCG	CTT	AAA	ACT	TTC	GCC	AGT	CGG	CGT	1200
Leu	Gly	Gly	Gln	His	Arg	Leu	Ser	Leu	Lys	Thr	Phe	Ala	Ser	Arg	Arg	
385				390					395					400		
GAG	TTT	GAA	AAC	TTA	AAC	CGC	GAC	GAT	TAT	TAC	TTC	AGC	GAA	AGA	GTA	1248
Glu	Phe	Glu	Asn	Leu	Asn	Arg	Asp	Asp	Tyr	Tyr	Phe	Ser	Glu	Arg	Val	
			405					410					415			
TCC	CGT	ACT	ACC	AGC	TCG	ATT	CAA	CAC	CCC	GTG	AAA	ACC	ACT	AAT	TAT	1296
Ser	Arg	Thr	Thr	Ser	Ser	Ile	Gln	His	Pro	Val	Lys	Thr	Thr	Asn	Tyr	
			420					425					430			
GGT	TTC	TCA	CTG	TCT	GAT	CAA	ATC	CAA	TGG	AAC	GAC	GTG	TTC	AGC	AGC	1344
Gly	Phe	Ser	Leu	Ser	Asp	Gln	Ile	Gln	Trp	Asn	Asp	Val	Phe	Ser	Ser	
		435				440					445					
CGT	GCA	GAT	ATC	CGT	TAC	GAT	CAT	ACC	AAA	ATG	ACG	CCT	CAG	GAA	TTG	1392
Arg	Ala	Asp	Ile	Arg	Tyr	Asp	His	Thr	Lys	Met	Thr	Pro	Gln	Glu	Leu	
	450					455					460					
AAT	GCC	GAG	TGT	CAT	GCT	TGT	GAC	AAA	ACA	CCG	CCT	GCA	GCC	AAT	ACT	1440
Asn	Ala	Glu	Cys	His	Ala	Cys	Asp	Lys	Thr	Pro	Pro	Ala	Ala	Asn	Thr	

B1
Cont

465	470	475	480	
TAT AAA GGC TGG AGC GGA TTT GTC GGT TTG GCG GCG CAA CTG AAT CAG				1488
Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Asn Gln	485	490	495	
GCT TGG CAT GTC GGT TAC GAC ATT ACT TCC GGC TAC CGT GTC CCC AAT				1536
Ala Trp His Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val Pro Asn	500	505	510	
GCG TCC GAA GTG TAT TTC ACT TAC AAC CAC GGT TCG GGT AAT TGG CTG				1584
Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn Trp Leu	515	520	525	
CCC AAT CCC AAC CTG AAA GCC GAG CGC AGC ACC ACC CAC ACC CTG TCT				1632
Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu Ser	530	535	540	
CTG CAA GGC CGC AGC GAA AAA GGT ACT TTG GAT GCC AAC CTG TAT CAA				1680
Leu Gln Gly Arg Ser Glu Lys Gly Thr Leu Asp Ala Asn Leu Tyr Gln	545	550	555	560
AGC AAT TAC CGA AAC TTC TTG TCT GAA GAG CAG AAG CTG ACC ACC AGC				1728
Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr Thr Ser	565	570	575	
GGC GAT GTC GGC TGT ACT CAG ATG AAT TAC TAC TAC GGT ATG TGT AGC				1776
Gly Asp Val Gly Cys Thr Gln Met Asn Tyr Tyr Tyr Gly Met Cys Ser	580	585	590	
AAT CCT TAT TCC GAA AAA CCG GAA TGG CAG ATG CAA AAT ATC GAT AAG				1824
Asn Pro Tyr Ser Glu Lys Pro Glu Trp Gln Met Gln Asn Ile Asp Lys	595	600	605	
GCC CGA ATC CGT GGT CTT GAG CTG ACG GGC CGT CTG AAT GTG ACA AAA				1872
Ala Arg Ile Arg Gly Leu Glu Leu Thr Gly Arg Leu Asn Val Thr Lys	610	615	620	
GTA GCG TCT TTT GTT CCT GAG GGC TGG AAA TTG TTC GGC TCG CTG GGT				1920
Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu Gly	625	630	635	640
TAT GCG AAA AGC AAA CTG TCG GGC GAC AAC AGC CTG CTG TCC ACA CAG				1968
Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr Gln	645	650	655	
CCG CCG AAA GTG ATT GCC GGT ATC GAC TAT GAA AGT CCG AGC GAA AAA				2016
Pro Pro Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu Lys	660	665	670	
TGG GGT GTG TTC TCC CGC CTG ACT TAT CTG GGT GCG AAA AAG GTC AAA				2064
Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val Lys	675	680	685	
GAC GCG CAA TAC ACC GTT TAT GAA AAC AAG GGC CGG GGT ACG CCT TTG				2112
Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Arg Gly Thr Pro Leu	690	695	700	

B1
cont

CAG AAA AAG GTA AAA GAT TAC CCG TGG CTG AAC AAG TCG GCT TAT GTG	2160
Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr Val	
705 710 715 720	
TTT GAT ATG TAC GGC TTC TAC AAA CTG GCT AAA AAC CTG ACT TTG CGT	2208
Phe Asp Met Tyr Gly Phe Tyr Lys Leu Ala Lys Asn Leu Thr Leu Arg	
725 730 735	
GCA GGC GTA TAT AAT GTG TTC AAC CGC AAA TAC ACC ACT TGG GAT TCC	2256
Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp Asp Ser	
740 745 750	
CTG CGC GGT TTG TAT AGC TAC ACC ACC ACC AAC GCG GTC GAC CGA GAT	2304
Leu Arg Gly Leu Tyr Ser Tyr Thr Thr Thr Asn Ala Val Asp Arg Asp	
755 760 765	
GGC AAA GGC TTA GAC CGC TAC CGC GCC TCA GGC CGT AAT TAC GCC GTA	2352
Gly Lys Gly Leu Asp Arg Tyr Arg Ala Ser Gly Arg Asn Tyr Ala Val	
770 775 780	
TCG CTG GAT TGG AAG TTT TGAATTCC	2378
Ser Leu Asp Trp Lys Phe	
885 790	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Lys Pro Leu His Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
1 5 10 15

Phe Gly Asn Pro Val Leu Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
20 25 30

Pro Val Lys Ala Glu Ile Lys Glu Val Arg Val Lys Asp Gln Leu Asn
35 40 45

Ala Pro Ala Thr Val Glu Arg Val Asn Leu Gly Arg Ile Gln Gln Glu
50 55 60

Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65 70 75 80

Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
85 90 95

Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Ser Leu Pro Asp
100 105 110

Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser

B1
cont

115	120	125
Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Glu Ile Ala Lys		
130	135	140
Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Gly Val		
145	150	155
Asn Tyr Gln Thr Leu Gln Gly His Asp Leu Leu Leu Asp Asp Arg Gln		
165	170	175
Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp		
180	185	190
Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala		
195	200	205
Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Glu		
210	215	220
Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Ile Ile Arg Gly		
225	230	235
Ser Ser Arg Gly Ile Pro Asp Pro Ser Lys His Lys Tyr His Asn Phe		
245	250	255
Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Lys His Arg Ile Gly Pro		
260	265	270
Ser Phe Asn Gly Gln Gln Gly His Asn Tyr Thr Ile Glu Glu Ser Tyr		
275	280	285
Asn Leu Thr Ala Ser Ser Trp Arg Glu Ala Asp Asp Val Asn Arg Arg		
290	295	300
Arg Asn Ala Asn Leu Phe Tyr Glu Trp Thr Pro Asp Ser Asn Trp Leu		
305	310	315
Ser Ser Leu Lys Ala Asp Phe Asp Tyr Gln Thr Thr Lys Val Ala Ala		
325	330	335
Val Asn Asn Lys Gly Ser Phe Pro Thr Asp Tyr Ser Thr Leu Thr Arg		
340	345	350
Asn Tyr Asn Gln Lys Asp Leu Glu Asn Ile Tyr Asn Arg Ser Met Asp		
355	360	365
Thr Arg Phe Lys Arg Phe Thr Leu Arg Met Asp Ser Gln Pro Leu Gln		
370	375	380
Leu Gly Gly Gln His Arg Leu Ser Leu Lys Thr Phe Ala Ser Arg Arg		
385	390	395
Glu Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Glu Arg Val		
405	410	415
Ser Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr Asn Tyr		
420	425	430

B1
Cant

Gly	Phe	Ser	Leu	Ser	Asp	Gln	Ile	Gln	Trp	Asn	Asp	Val	Phe	Ser	Ser
		435					440					445			
Arg	Ala	Asp	Ile	Arg	Tyr	Asp	His	Thr	Lys	Met	Thr	Pro	Gln	Glu	Leu
		450				455					460				
Asn	Ala	Glu	Cys	His	Ala	Cys	Asp	Lys	Thr	Pro	Pro	Ala	Ala	Asn	Thr
465					470					475				480	
Tyr	Lys	Gly	Trp	Ser	Gly	Phe	Val	Gly	Leu	Ala	Ala	Gln	Leu	Asn	Gln
				485					490					495	
Ala	Trp	His	Val	Gly	Tyr	Asp	Ile	Thr	Ser	Gly	Tyr	Arg	Val	Pro	Asn
			500					505					510		
Ala	Ser	Glu	Val	Tyr	Phe	Thr	Tyr	Asn	His	Gly	Ser	Gly	Asn	Trp	Leu
		515					520					525			
Pro	Asn	Pro	Asn	Leu	Lys	Ala	Glu	Arg	Ser	Thr	Thr	His	Thr	Leu	Ser
		530				535					540				
Leu	Gln	Gly	Arg	Ser	Glu	Lys	Gly	Thr	Leu	Asp	Ala	Asn	Leu	Tyr	Gln
545					550					555					560
Ser	Asn	Tyr	Arg	Asn	Phe	Leu	Ser	Glu	Glu	Gln	Lys	Leu	Thr	Thr	Ser
				565						570				575	
Gly	Asp	Val	Gly	Cys	Thr	Gln	Met	Asn	Tyr	Tyr	Tyr	Gly	Met	Cys	Ser
			580					585					590		
Asn	Pro	Tyr	Ser	Glu	Lys	Pro	Glu	Trp	Gln	Met	Gln	Asn	Ile	Asp	Lys
		595					600					605			
Ala	Arg	Ile	Arg	Gly	Leu	Glu	Leu	Thr	Gly	Arg	Leu	Asn	Val	Thr	Lys
		610				615					620				
Val	Ala	Ser	Phe	Val	Pro	Glu	Gly	Trp	Lys	Leu	Phe	Gly	Ser	Leu	Gly
625					630					635					640
Tyr	Ala	Lys	Ser	Lys	Leu	Ser	Gly	Asp	Asn	Ser	Leu	Leu	Ser	Thr	Gln
				645					650					655	
Pro	Pro	Lys	Val	Ile	Ala	Gly	Ile	Asp	Tyr	Glu	Ser	Pro	Ser	Glu	Lys
			660					665					670		
Trp	Gly	Val	Phe	Ser	Arg	Leu	Thr	Tyr	Leu	Gly	Ala	Lys	Lys	Val	Lys
		675					680					685			
Asp	Ala	Gln	Tyr	Thr	Val	Tyr	Glu	Asn	Lys	Gly	Arg	Gly	Thr	Pro	Leu
		690				695					700				
Gln	Lys	Lys	Val	Lys	Asp	Tyr	Pro	Trp	Leu	Asn	Lys	Ser	Ala	Tyr	Val
705					710					715					720
Phe	Asp	Met	Tyr	Gly	Phe	Tyr	Lys	Leu	Ala	Lys	Asn	Leu	Thr	Leu	Arg
				725					730					735	
Ala	Gly	Val	Tyr	Asn	Val	Phe	Asn	Arg	Lys	Tyr	Thr	Thr	Trp	Asp	Ser
			740					745					750		

B!
Cont

Leu Arg Gly Leu Tyr Ser Tyr Thr Thr Thr Asn Ala Val Asp Arg Asp
 755 760 765
 Gly Lys Gly Leu Asp Arg Tyr Arg Ala Ser Gly Arg Asn Tyr Ala Val
 770 775 780
 Ser Leu Asp Trp Lys Phe
 785 790

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Gln Gln Gln His Leu Phe Arg Leu Asn Ile Leu Cys Leu Ser Leu
 1 5 10 15
 Met Thr Ala Leu Pro Val Tyr Ala Glu Asn Val Gln Ala Glu Gln Ala
 20 25 30
 Gln Glu Lys Gln Leu Asp Thr Ile Val Lys Ala Lys Lys Gln Lys Thr
 35 40 45
 Arg Arg Asp Asn Glu Val Thr Gly Leu Gly Lys Leu Val Lys Ser Ser
 50 55 60
 Asp Thr Leu Ser Lys Glu Gln Val Leu Asn Ile Arg Asp Leu Thr Arg
 65 70 75 80
 Tyr Asp Pro Gly Ile Ala Val Val Glu Gln Gly Arg Gly Ala Ser Ser
 85 90 95
 Gly Tyr Ser Ile Arg Gly Met Asp Lys Asn Arg Val Ser Leu Thr Val
 100 105 110
 Asp Gly Val Ser Gln Ile Gln Ser Tyr Thr Ala Gln Ala Ala Leu Gly
 115 120 125
 Gly Thr Arg Thr Ala Gly Ser Ser Gly Ala Ile Asn Glu Ile Glu Tyr
 130 135 140
 Glu Asn Val Lys Ala Val Glu Ile Ser Lys Gly Ser Asn Ser Ser Glu
 145 150 155 160
 Tyr Gly Asn Gly Ala Leu Ala Gly Ser Val Ala Phe Gln Thr Lys Thr
 165 170 175
 Ala Ala Asp Ile Ile Gly Glu Gly Lys Gln Trp Gly Ile Gln Ser Lys
 180 185 190
 Thr Ala Tyr Ser Gly Lys Asp His Ala Leu Thr Gln Ser Leu Ala Leu
 195 200 205

B1
 Cont

Ala Gly Arg Ser Gly Gly Ala Glu Ala Leu Leu Ile Tyr Thr Lys Arg
210 215 220

Arg Gly Arg Glu Ile His Ala His Lys Asp Ala Gly Lys Gly Val Gln
225 230 235 240

Ser Phe Asn Arg Leu Pro Ile Cys Arg Phe Gly Asn Asn Thr Tyr Thr
245 250 255

Asp Cys Thr Pro Arg Asn Ile Gly Gly Asn Gly Tyr Tyr Ala Ala Val
260 265 270

Gln Asp Asn Val Arg Leu Gly Arg Trp Ala Asp Val Gly Ala Gly Ile
275 280 285

Arg Tyr Asp Tyr Arg Ser Thr His Ser Glu Asp Lys Ser Val Ser Thr
290 295 300

Gly Thr His Arg Asn Leu Ser Trp Asn Ala Gly Val Val Leu Lys Pro
305 310 315 320

Phe Thr Trp Met Asp Leu Thr Tyr Arg Ala Ser Thr Gly Phe Arg Leu
325 330 335

Pro Ser Phe Ala Glu Met Tyr Gly Trp Arg Ala Gly Glu Ser Leu Lys
340 345 350

Thr Leu Asp Leu Lys Pro Glu Lys Ser Phe Asn Arg Glu Ala Gly Ile
355 360 365

Val Phe Lys Gly Asp Phe Gly Asn Leu Glu Ala Ser Tyr Phe Asn Asn
370 375 380

Ala Tyr Arg Asp Leu Ile Ala Phe Gly Tyr Glu Thr Arg Thr Gln Asn
385 390 395 400

Gly Gln Thr Ser Ala Ser Gly Asp Pro Gly Tyr Arg Asn Ala Gln Asn
405 410 415

Ala Arg Ile Ala Gly Ile Asn Ile Leu Gly Lys Ile Asp Trp His Gly
420 425 430

Val Trp Gly Gly Leu Pro Asp Gly Leu Tyr Ser Thr Leu Ala Tyr Asn
435 440 445

Arg Ile Lys Val Lys Asp Ala Asp Arg Ala Asp Arg Thr Phe Val Thr
450 455 460

Ser Tyr Leu Phe Asp Ala Val Gln Pro Ser Arg Tyr Val Leu Gly Leu
465 470 475 480

Gly Tyr Asp His Pro Asp Gly Ile Trp Gly Ile Asn Thr Met Phe Thr
485 490 495

Tyr Ser Lys Ala Lys Ser Val Asp Glu Leu Leu Gly Ser Gln Ala Leu
500 505 510

Leu Asn Gly Asn Ala Asn Ala Lys Lys Ala Ala Ser Arg Arg Thr Arg
515 520 525

Pl
cont

Pro Trp Tyr Val Thr Asp Val Ser Gly Tyr Tyr Asn Ile Lys Lys His
 530 535 540

Leu Thr Leu Arg Ala Gly Val Tyr Asn Leu Leu Asn Tyr Arg Tyr Val
 545 550 555 560

Thr Trp Glu Asn Val Arg Gln Thr Ala Gly Gly Ala Val Asn Gln His
 565 570 575

Lys Asn Val Gly Val Tyr Asn Arg Tyr Ala Ala Pro Gly Arg Asn Tyr
 580 585 590

Thr Phe Ser Leu Glu Met Lys Phe
 595 600

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Asn Lys Lys His Gly Phe Gln Leu Thr Leu Thr Ala Leu Ala Val
 1 5 10 15

Ala Ala Ala Phe Pro Ser Tyr Ala Ala Asn Pro Glu Thr Ala Ala Pro
 20 25 30

Asp Ala Ala Gln Thr Gln Ser Leu Lys Glu Val Thr Val Arg Ala Ala
 35 40 45

Lys Val Gly Arg Arg Ser Lys Glu Ala Thr Gly Leu Gly Lys Ile Ala
 50 55 60

Lys Thr Ser Glu Thr Leu Asn Lys Glu Gln Val Leu Gly Ile Arg Asp
 65 70 75 80

Leu Thr Arg Tyr Asp Pro Gly Val Ala Val Val Glu Gln Gly Asn Gly
 85 90 95

Ala Ser Gly Glu Tyr Ser Ile Arg Gly Val Asp Lys Asn Arg Val Ala
 100 105 110

Val Ser Val Asp Gly Val Ala Gln Ile Gln Ala Phe Thr Val Gln Gly
 115 120 125

Ser Leu Ser Gly Tyr Gly Gly Arg Gly Gly Ser Gly Ala Ile Asn Glu
 130 135 140

Ile Glu Tyr Glu Asn Ile Ser Thr Val Glu Ile Asp Lys Gly Ala Gly
 145 150 155 160

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 Cont

Ser	Ser	Asp	His	Gly	Ser	Gly	Ala	Leu	Gly	Gly	Ala	Val	Ala	Phe	Arg	165	170	175
Thr	Lys	Glu	Ala	Ala	Asp	Leu	Ile	Ser	Asp	Gly	Lys	Ser	Trp	Gly	Ile	180	185	190
Gln	Ala	Lys	Thr	Ala	Tyr	Gly	Ser	Lys	Asn	Arg	Gln	Phe	Met	Lys	Ser	195	200	205
Leu	Gly	Ala	Gly	Phe	Ser	Lys	Asp	Gly	Trp	Glu	Gly	Leu	Leu	Ile	Arg	210	215	220
Thr	Glu	Arg	Gln	Gly	Arg	Glu	Thr	His	Pro	His	Gly	Asp	Ile	Ala	Asp	225	230	235
Gly	Val	Ala	Tyr	Gly	Ile	Asn	Arg	Leu	Ser	Val	Cys	Gly	Tyr	Ile	Glu	245	250	255
Thr	Leu	Arg	Ser	Arg	Lys	Cys	Val	Pro	Arg	Lys	Ile	Asn	Gly	Ser	Asn	260	265	270
Ile	His	Ile	Ser	Leu	Asn	Asp	Arg	Phe	Ser	Ile	Gly	Lys	Tyr	Phe	Asp	275	280	285
Phe	Ser	Leu	Gly	Gly	Arg	Tyr	Asp	Arg	Lys	Asn	Phe	Thr	Thr	Ser	Glu	290	295	300
Glu	Leu	Val	Arg	Ser	Gly	Arg	Tyr	Val	Asp	Arg	Ser	Trp	Asn	Ser	Gly	305	310	315
Ile	Val	Phe	Lys	Pro	Asn	Arg	His	Phe	Ser	Leu	Ser	Tyr	Arg	Ala	Ser	325	330	335
Ser	Gly	Phe	Arg	Thr	Pro	Ser	Phe	Gln	Glu	Leu	Phe	Gly	Ile	Asp	Ile	340	345	350
Tyr	His	Asp	Tyr	Pro	Lys	Gly	Trp	Gln	Arg	Pro	Ala	Leu	Lys	Ser	Glu	355	360	365
Lys	Ala	Ala	Asn	Arg	Glu	Ile	Gly	Leu	Gln	Trp	Lys	Gly	Asp	Phe	Gly	370	375	380
Phe	Leu	Glu	Ile	Ser	Ser	Phe	Arg	Asn	Arg	Tyr	Thr	Asp	Met	Ile	Ala	385	390	395
Val	Ala	Asp	His	Lys	Thr	Lys	Leu	Pro	Asn	Gln	Ala	Gly	Gln	Leu	Thr	405	410	415
Glu	Ile	Asp	Ile	Arg	Asp	Tyr	Tyr	Asn	Ala	Gln	Asn	Met	Ser	Leu	Gln	420	425	430
Gly	Val	Asn	Ile	Leu	Gly	Lys	Ile	Asp	Trp	Asn	Gly	Val	tyr	Gly	Lys	435	440	445
Leu	Pro	Glu	Gly	Leu	Tyr	Thr	Thr	Leu	Ala	Tyr	Asn	Arg	Ile	Lys	Pro	450	455	460
Lys	Ser	Val	Ser	Asn	Arg	Pro	Gly	Leu	Ser	Leu	Arg	Ser	Tyr	Ala	Leu	465	470	475

B1
Cont.

Asp	Ala	Val	Gln	Pro	Ser	Arg	Tyr	Val	Leu	Gly	Phe	Gly	Tyr	Asp	Gln
				485					490					495	
Pro	Glu	Gly	Lys	Trp	Gly	Ala	Asn	Ile	Met	Leu	Thr	Tyr	Ser	Lys	Gly
			500					505					510		
Lys	Asn	Pro	Asp	Glu	Leu	Ala	Tyr	Leu	Ala	Gly	Asp	Gln	Lys	Arg	Tyr
		515					520					525			
Ser	Thr	Lys	Arg	Ala	Ser	Ser	Ser	Trp	Ser	Thr	Ala	Asp	Val	Ser	Ala
	530					535					540				
Tyr	Leu	Asn	Leu	Lys	Lys	Arg	Leu	Thr	Leu	Arg	Ala	Ala	Ile	Tyr	Asn
545				550					555						560
Ile	Gly	Asn	Tyr	Arg	Tyr	Val	Thr	Trp	Glu	Ser	Leu	Arg	Gln	Thr	Ala
				565					570					575	
Glu	Ser	Thr	Ala	Asn	Arg	His	Gly	Gly	Asp	Ser	Asn	Tyr	Gly	Arg	Tyr
			580					585					590		
Ala	Ala	Pro	Gly	Arg	Asn	Phe	Ser	Leu	Ala	Leu	Gly	Met	Lys	Phe	
		595					600					605			

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAACAGGTCT CGGCATAG

18

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCGAATTCA AACAGGTCTC GGCATAG

27

(2) INFORMATION FOR SEQ ID NO:13:

B1
Cont

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGCGAATTCA AAAACTTCCA TTCCAGCGAT ACG

33

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TAAAACTTCC ATTCCAGCGA TACG

24

2) INFORMATION FOR SEQ ID NO:15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: peptide
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Glu Thr Thr Pro Val Lys Ala
5

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 792 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Lys Pro Leu Gln Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
1 5 10 15

Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr

B1
Cont

20					25					30					
Pro	Val	Lys	Ala	Glu	Val	Lys	Ala	Val	Arg	Val	Lys	Gly	Gln	Arg	Asn
	35						40					45			
Ala	Pro	Ala	Ala	Val	Glu	Arg	Val	Asn	Leu	Asn	Arg	Ile	Lys	Gln	Glu
	50					55					60				
Met	Ile	Arg	Asp	Asn	Lys	Asp	Leu	Val	Arg	Tyr	Ser	Thr	Asp	Val	Gly
	65					70					75				80
Leu	Ser	Asp	Ser	Gly	Arg	His	Gln	Lys	Gly	Phe	Ala	Val	Arg	Gly	Val
				85					90					95	
Glu	Gly	Asn	Arg	Val	Gly	Val	Ser	Ile	Asp	Gly	Val	Asn	Leu	Pro	Asp
			100					105					110		
Ser	Glu	Glu	Asn	Ser	Leu	Tyr	Ala	Arg	Tyr	Gly	Asn	Phe	Asn	Ser	Ser
		115					120					125			
Arg	Leu	Ser	Ile	Asp	Pro	Glu	Leu	Val	Arg	Asn	Ile	Asp	Ile	Val	Lys
	130					135					140				
Gly	Ala	Asp	Ser	Phe	Asn	Thr	Gly	Ser	Gly	Ala	Leu	Gly	Gly	Gly	Val
	145					150					155				160
Asn	Tyr	Gln	Thr	Leu	Gln	Gly	Arg	Asp	Leu	Leu	Leu	Pro	Glu	Arg	Gln
				165					170					175	
Phe	Gly	Val	Met	Met	Lys	Asn	Gly	Tyr	Ser	Thr	Arg	Asn	Arg	Glu	Trp
			180					185					190		
Thr	Asn	Thr	Leu	Gly	Phe	Gly	Val	Ser	Asn	Asp	Arg	Val	Asp	Ala	Ala
		195					200						205		
Leu	Leu	Tyr	Ser	Gln	Arg	Arg	Gly	His	Glu	Thr	Glu	Ser	Ala	Gly	Lys
	210					215					220				
Arg	Gly	Tyr	Pro	Val	Glu	Gly	Ala	Gly	Ser	Gly	Ala	Asn	Ile	Arg	Gly
	225					230					235				240
Ser	Ala	Arg	Gly	Ile	Pro	Asp	Pro	Ser	Gln	His	Lys	Tyr	His	Ser	Phe
				245					250					255	
Leu	Gly	Lys	Ile	Ala	Tyr	Gln	Ile	Asn	Asp	Asn	His	Arg	Ile	Gly	Ala
			260					265					270		
Ser	Leu	Asn	Gly	Gln	Gln	Gly	His	Asn	Tyr	Thr	Val	Glu	Glu	Ser	Tyr
		275					280					285			
Asn	Leu	Leu	Ala	Ser	Tyr	Trp	Arg	Glu	Ala	Asp	Asp	Val	Asn	Arg	Arg
	290					295					300				
Arg	Asn	Thr	Asn	Leu	Phe	Tyr	Glu	Trp	Thr	Pro	Glu	Ser	Asp	Arg	Leu
	305					310					315				320
Ser	Met	Val	Lys	Ala	Asp	Val	Asp	Tyr	Gln	Lys	Thr	Lys	Val	Ser	Ala
				325					330					335	

B1
Cont.

Val	Asn	Tyr	Lys	Gly	Ser	Phe	Pro	Ile	Glu	Asp	Ser	Ser	Thr	Leu	Thr	340	345	350	
Arg	Asn	Tyr	Asn	Gln	Lys	Asp	Leu	Asp	Glu	Ile	Tyr	Asn	Arg	Ser	Met	355	360	365	
Asp	Thr	Arg	Phe	Lys	Arg	Ile	Thr	Leu	Arg	Leu	Asp	Ser	His	Pro	Leu	370	375	380	
Gln	Leu	Gly	Gly	Gly	Arg	His	Arg	Leu	Ser	Phe	Lys	Thr	Phe	Ala	Ser	385	390	395	400
Arg	Arg	Asp	Phe	Glu	Asn	Leu	Asn	Arg	Asp	Asp	Tyr	Tyr	Phe	Ser	Gly	405	410	415	
Arg	Val	Val	Arg	Thr	Thr	Ser	Ser	Ile	Gln	His	Pro	Val	Lys	Thr	Thr	420	425	430	
Asn	Tyr	Gly	Phe	Ser	Leu	Ser	Asp	Gln	Ile	Gln	Trp	Asn	Asp	Val	Phe	435	440	445	
Ser	Ser	Arg	Ala	Gly	Ile	Arg	Tyr	Asp	His	Thr	Lys	Met	Thr	Pro	Gln	450	455	460	
Glu	Leu	Asn	Ala	Glu	Cys	His	Ala	Cys	Asp	Lys	Thr	Pro	Pro	Ala	Ala	465	470	475	480
Asn	Thr	Tyr	Lys	Gly	Trp	Ser	Gly	Phe	Val	Gly	Leu	Ala	Ala	Gln	Leu	485	490	495	
Asn	Gln	Ala	Trp	Arg	Val	Gly	Tyr	Asp	Ile	Thr	Ser	Gly	Tyr	Arg	Val	500	505	510	
Pro	Asn	Ala	Ser	Glu	Val	Tyr	Phe	Thr	Tyr	Asn	His	Gly	Ser	Gly	Asn	515	520	525	
Trp	Leu	Pro	Asn	Pro	Asn	Leu	Lys	Ala	Glu	Arg	Thr	Thr	Thr	His	Thr	530	535	540	
Leu	Ser	Leu	Gln	Gly	Arg	Ser	Glu	Lys	Gly	Thr	Leu	Asp	Ala	Asn	Leu	545	550	555	560
Tyr	Gln	Ser	Asn	Tyr	Arg	Asn	Phe	Leu	Ser	Glu	Glu	Gln	Lys	Leu	Thr	565	570	575	
Thr	Ser	Gly	Asp	Val	Ser	Cys	Thr	Gln	Met	Asn	Tyr	Tyr	Tyr	Gly	Met	580	585	590	
Cys	Ser	Asn	Pro	Tyr	Ser	Glu	Lys	Leu	Asp	Trp	Gln	Met	Gln	Asn	Ile	595	600	605	
Asp	Lys	Ala	Arg	Ile	Arg	Gly	Leu	Glu	Leu	Thr	Gly	Arg	Leu	Asn	Val	610	615	620	
Asp	Lys	Val	Ala	Ser	Phe	Val	Pro	Glu	Gly	Trp	Lys	Leu	Phe	Gly	Ser	625	630	635	640
Leu	Gly	Tyr	Ala	Lys	Ser	Lys	Leu	Ser	Gly	Asp	Asn	Ser	Leu	Leu	Ser				

B1
Cont

				645						650						655			
Thr	Gln	Pro	Leu	Lys	Val	Ile	Ala	Gly	Ile	Asp	Tyr	Glu	Ser	Pro	Ser				
			660					665					670						
Glu	Lys	Trp	Gly	Val	Phe	Ser	Arg	Leu	Thr	Tyr	Leu	Gly	Ala	Lys	Lys				
		675					680					685							
Val	Lys	Asp	Ala	Gln	Tyr	Thr	Val	Tyr	Glu	Asn	Lys	Gly	Trp	Gly	Thr				
		690				695					700								
Pro	Leu	Gln	Lys	Lys	Val	Lys	Asp	Tyr	Pro	Trp	Leu	Asn	Lys	Ser	Ala				
705					710					715					720				
Tyr	Val	Phe	Asp	Met	Tyr	Gly	Phe	Tyr	Lys	Pro	Val	Lys	Asn	Leu	Thr				
			725					730						735					
Leu	Arg	Ala	Gly	Val	Tyr	Asn	Val	Phe	Asn	Arg	Lys	Tyr	Thr	Thr	Trp				
		740					745						750						
Asp	Ser	Leu	Arg	Gly	Leu	Tyr	Ser	Tyr	Ser	Thr	Thr	Asn	Ser	Val	Asp				
		755					760					765							
Arg	Asp	Gly	Lys	Gly	Leu	Asp	Arg	Tyr	Arg	Ala	Pro	Ser	Arg	Asn	Tyr				
	770					775					780								
Ala	Val	Ser	Leu	Glu	Trp	Lys	Phe												
785					790														

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 791 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Lys Pro Leu Gln Met Pro Pro Ile Ala Ala Leu Leu Gly Ser Ile
 1 5 10 15

Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
 20 25 30

Pro Val Lys Ala Glu Val Lys Ala Val Arg Val Lys Gly Gln Arg Asn
 35 40 45

Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu
 50 55 60

Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
 65 70 75 80

*Pl
Cont*

B1
Cont

385		390		395		400
Arg Asp Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Gly Arg						
		405		410		415
Val Val Arg Thr Thr Asn Ser Ile Gln His Pro Val Lys Thr Thr Asn						
		420		425		430
Tyr Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser						
		435		440		445
Ser Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu						
		450		455		460
Leu Asn Ala Asp Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn						
		465		470		480
Thr Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Ser						
		485		490		495
Gln Thr Trp Arg Val Gly Tyr Asp Val Thr Ser Gly Phe Arg Val Pro						
		500		505		510
Asn Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Thr Trp						
		515		520		525
Lys Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu						
		530		535		540
Ser Leu Gln Gly Arg Gly Asp Lys Gly Thr Leu Asp Ala Asn Leu Tyr						
		545		550		560
Gln Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Asn Leu Thr Val						
		565		570		575
Ser Gly Thr Pro Gly Cys Thr Glu Glu Asp Ala Tyr Tyr Tyr Arg Cys						
		580		585		590
Ser Asp Pro Tyr Lys Glu Lys Leu Asp Trp Gln Met Lys Asn Ile Asp						
		595		600		605
Lys Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val Asp						
		610		615		620
Lys Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu						
		625		630		640
Gly Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr						
		645		650		655
Gln Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu						
		660		665		670
Lys Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val						
		675		680		685
Lys Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr Pro						
		690		695		700

B1
Cont.

Leu Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr
705 710 715 720

Val Phe Asp Met Tyr Gly Phe Tyr Lys Pro Ala Lys Asn Leu Thr Leu
725 730 735

Arg Ala Gly Val Tyr Asn Leu Phe Asn Arg Lys Tyr Thr Thr Trp Asp
740 745 750

Ser Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ala Val Asp Arg
755 760 765

Asp Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Gly Arg Asn Tyr Ala
770 775 780

Val Ser Leu Glu Trp Lys Phe
785 790

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Lys Pro Leu Gln Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
1 5 10 15

Phe Gly Asn Pro Val Leu Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
20 25 30

Pro Val Lys Ala Glu Ile Lys Ala Val Arg Val Lys Gly Gln Arg Asn
35 40 45

Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu
50 55 60

Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65 70 75 80

Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
85 90 95

Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp
100 105 110

Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
115 120 125

Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Glu Ile Val Lys
130 135 140

B1
Cont

Gly	Ala	Asp	Ser	Phe	Asn	Thr	Gly	Ser	Gly	Ala	Leu	Gly	Gly	Gly	Val	145	150	155	160
Asn	Tyr	Gln	Thr	Leu	Gln	Gly	Arg	Asp	Leu	Leu	Leu	Asp	Asp	Arg	Gln	165	170	175	
Phe	Gly	Val	Met	Met	Lys	Asn	Gly	Tyr	Ser	Thr	Arg	Asn	Arg	Glu	Trp	180	185	190	
Thr	Asn	Thr	Leu	Gly	Phe	Gly	Val	Ser	Asn	Asp	Arg	Val	Asp	Ala	Ala	195	200	205	
Leu	Leu	Tyr	Ser	Gln	Arg	Arg	Gly	His	Glu	Thr	Glu	Ser	Ala	Gly	Asn	210	215	220	
Arg	Gly	Tyr	Pro	Val	Glu	Gly	Ala	Gly	Lys	Glu	Thr	Asn	Ile	Arg	Gly	225	230	235	240
Ser	Ala	Arg	Gly	Ile	Pro	Asp	Pro	Ser	Lys	His	Lys	Tyr	His	Asn	Phe	245	250	255	
Leu	Gly	Lys	Ile	Ala	Tyr	Gln	Ile	Asn	Asp	Asn	His	Arg	Ile	Gly	Ala	260	265	270	
Ser	Leu	Asn	Gly	Gln	Gln	Gly	His	Asn	Tyr	Thr	Val	Glu	Glu	Ser	Tyr	275	280	285	
Asn	Leu	Thr	Ala	Ser	Ser	Trp	Arg	Glu	Ala	Asp	Asp	Val	Asn	Arg	Arg	290	295	300	
Arg	Asn	Ala	Asn	Leu	Phe	Tyr	Glu	Trp	Met	Pro	Asp	Ser	Asn	Trp	Leu	305	310	315	320
Ser	Ser	Leu	Lys	Ala	Asp	Phe	Asp	Tyr	Gln	Lys	Thr	Lys	Val	Ala	Ala	325	330	335	
Ile	Asn	Lys	Gly	Ser	Phe	Pro	Thr	Asn	Tyr	Thr	Thr	Trp	Glu	Thr	Glu	340	345	350	
Tyr	His	Lys	Lys	Glu	Val	Gly	Glu	Ile	Tyr	Asn	Arg	Ser	Met	Asp	Thr	355	360	365	
Arg	Phe	Lys	Arg	Phe	Thr	Leu	Arg	Leu	Asp	Ser	His	Pro	Leu	Gln	Leu	370	375	380	
Gly	Gly	Gly	Arg	His	Arg	Leu	Ser	Phe	Lys	Thr	Phe	Ala	Ser	Arg	Arg	385	390	395	400
Asp	Phe	Glu	Asn	Leu	Asn	Arg	Asp	Asp	Tyr	Tyr	Phe	Ser	Gly	Arg	Val	405	410	415	
Val	Arg	Thr	Thr	Ser	Ser	Ile	Gln	His	Pro	Val	Lys	Thr	Thr	Asn	Tyr	420	425	430	
Gly	Phe	Ser	Leu	Ser	Asp	Gln	Ile	Gln	Trp	Asn	Asp	Val	Phe	Ser	Ser	435	440	445	
Arg	Ala	Gly	Ile	Arg	Tyr	Asp	His	Thr	Lys	Met	Thr	Pro	Gln	Glu	Leu	450	455	460	

B1
cont

Asn	Ala	Glu	Cys	His	Ala	Cys	Asp	Lys	Thr	Pro	Pro	Ala	Ala	Asn	Thr
465					470					475					480
Tyr	Lys	Gly	Trp	Ser	Gly	Phe	Val	Gly	Leu	Ala	Ala	Gln	Leu	Asn	Gln
				485					490					495	
Ala	Trp	Arg	Val	Gly	Tyr	Asp	Ile	Thr	Ser	Gly	Tyr	Arg	Val	Pro	Asn
			500					505					510		
Ala	Ser	Glu	Val	Tyr	Phe	Thr	Tyr	Asn	His	Gly	Ser	Gly	Asn	Trp	Leu
		515					520					525			
Pro	Asn	Pro	Asn	Leu	Lys	Ala	Glu	Arg	Ser	Thr	Thr	His	Thr	Leu	Ser
	530					535					540				
Leu	Gln	Gly	Arg	Ser	Glu	Lys	Gly	Met	Leu	Asp	Ala	Asn	Leu	Tyr	Gln
545					550					555					560
Ser	Asn	Tyr	Arg	Asn	Phe	Leu	Ser	Glu	Glu	Gln	Lys	Leu	Thr	Thr	Ser
				565					570					575	
Gly	Thr	Pro	Gly	Cys	Thr	Glu	Glu	Asn	Ala	Tyr	Tyr	Ser	Ile	Cys	Ser
			580					585					590		
Asp	Pro	Tyr	Lys	Glu	Lys	Leu	Asp	Trp	Gln	Met	Lys	Asn	Ile	Asp	Lys
		595					600					605			
Ala	Arg	Ile	Arg	Gly	Ile	Glu	Leu	Thr	Gly	Arg	Leu	Asn	Val	Asp	Lys
		610				615					620				
Val	Ala	Ser	Phe	Val	Pro	Glu	Gly	Trp	Lys	Leu	Phe	Gly	Ser	Leu	Gly
625					630					635					640
Tyr	Ala	Lys	Ser	Lys	Leu	Ser	Gly	Asp	Asn	Ser	Leu	Leu	Ser	Thr	Gln
				645					650					655	
Pro	Leu	Lys	Val	Ile	Ala	Gly	Ile	Asp	Tyr	Glu	Ser	Pro	Ser	Glu	Lys
			660					665					670		
Trp	Gly	Val	Phe	Ser	Arg	Leu	Thr	Tyr	Leu	Gly	Ala	Lys	Lys	Val	Lys
		675					680					685			
Asp	Ala	Gln	Tyr	Thr	Val	Tyr	Glu	Asn	Lys	Gly	Trp	Gly	Thr	Pro	Leu
		690				695					700				
Gln	Lys	Lys	Val	Lys	Asp	Tyr	Pro	Trp	Leu	Asn	Lys	Ser	Ala	Tyr	Val
705					710					715					720
Phe	Asp	Met	Tyr	Gly	Phe	Tyr	Lys	Pro	Val	Lys	Asn	Leu	Thr	Leu	Arg
				725					730					735	
Ala	Gly	Val	Tyr	Asn	Leu	Phe	Asn	Arg	Lys	Tyr	Thr	Thr	Trp	Asp	Ser
			740					745					750		
Leu	Arg	Gly	Leu	Tyr	Ser	Tyr	Ser	Thr	Thr	Asn	Ala	Val	Asp	Arg	Asp
		755					760					765			
Gly	Lys	Gly	Leu	Asp	Arg	Tyr	Arg	Ala	Pro	Gly	Arg	Asn	Tyr	Ala	Val
		770				775					780				

B1
Cont

Ser Leu Glu Trp Lys Phe
785 790

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Lys Pro Leu His Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
1 5 10 15
Phe Gly Asn Pro Val Leu Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
20 25 30
Pro Val Lys Ala Glu Ile Lys Glu Val Arg Val Lys Asp Gln Leu Asn
35 40 45
Ala Pro Ala Thr Val Glu Arg Val Asn Leu Gly Arg Ile Gln Gln Glu
50 55 60
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65 70 75 80
Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
85 90 95
Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Ser Leu Pro Asp
100 105 110
Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
115 120 125
Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Glu Ile Ala Lys
130 135 140
Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Gly Val
145 150 155 160
Asn Tyr Gln Thr Leu Gln Gly His Asp Leu Leu Leu Asp Asp Arg Gln
165 170 175
Phe Gly Val Met Met Lys Asn Gly Tyr Ser Ser Arg Asn Arg Glu Trp
180 185 190
Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
195 200 205
Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Glu
210 215 220

B1
Cont

Arg	Gly	Tyr	Pro	Val	Glu	Gly	Ala	Gly	Ser	Gly	Ala	Ile	Ile	Arg	Gly	225	230	235	240
Ser	Ser	Arg	Gly	Ile	Pro	Asp	Pro	Ser	Lys	His	Lys	Tyr	His	Asn	Phe	245	250	255	
Leu	Gly	Lys	Ile	Ala	Tyr	Gln	Ile	Asn	Asp	Lys	His	Arg	Ile	Gly	Pro	260	265	270	
Ser	Phe	Asn	Gly	Gln	Gln	Gly	His	Asn	Tyr	Thr	Ile	Glu	Glu	Ser	Tyr	275	280	285	
Asn	Leu	Thr	Ala	Ser	Ser	Trp	Arg	Glu	Ala	Asp	Asp	Val	Asn	Arg	Arg	290	295	300	
Arg	Asn	Ala	Asn	Leu	Phe	Tyr	Glu	Trp	Thr	Pro	Asp	Ser	Asn	Trp	Leu	305	310	315	320
Ser	Ser	Leu	Lys	Ala	Asp	Phe	Asp	Tyr	Gln	Thr	Thr	Lys	Val	Ala	Ala	325	330	335	
Val	Asn	Asn	Lys	Gly	Ser	Phe	Pro	Thr	Asp	Tyr	Ser	Thr	Trp	Thr	Arg	340	345	350	
Asn	Tyr	Asn	Gln	Lys	Asp	Leu	Glu	Asn	Ile	Tyr	Asn	Arg	Ser	Met	Asp	355	360	365	
Thr	Arg	Phe	Lys	Arg	Phe	Thr	Leu	Arg	Met	Asp	Ser	Gln	Pro	Leu	Gln	370	375	380	
Leu	Gly	Gly	Arg	His	Arg	Leu	Ser	Leu	Lys	Thr	Phe	Ala	Ser	Arg	Arg	385	390	395	400
Glu	Phe	Glu	Asn	Leu	Asn	Arg	Asp	Asp	Tyr	Tyr	Phe	Ser	Glu	Arg	Val	405	410	415	
Ser	Arg	Thr	Thr	Ser	Ser	Ile	Gln	His	Pro	Val	Lys	Thr	Thr	Asn	Tyr	420	425	430	
Gly	Phe	Ser	Leu	Ser	Asp	Gln	Ile	Gln	Trp	Asn	Asp	Val	Phe	Ser	Ser	435	440	445	
Arg	Ala	Asp	Ile	Arg	Tyr	Asp	His	Thr	Lys	Met	Thr	Pro	Gln	Glu	Leu	450	455	460	
Asn	Ala	Asp	Cys	His	Ala	Cys	Asp	Lys	Thr	Pro	Pro	Ala	Ala	Asn	Thr	465	470	475	480
Tyr	Lys	Gly	Trp	Ser	Gly	Phe	Val	Gly	Leu	Ala	Ala	Gln	Leu	Asn	Gln	485	490	495	
Ala	Trp	His	Val	Gly	Tyr	Asp	Ile	Thr	Ser	Gly	Tyr	Arg	Val	Pro	Asn	500	505	510	
Ala	Ser	Glu	Val	Tyr	Phe	Thr	Tyr	Asn	His	Gly	Ser	Gly	Asn	Trp	Leu	515	520	525	
Pro	Asn	Pro	Asn	Leu	Lys	Ala	Glu	Arg	Ser	Thr	Thr	His	Thr	Leu	Ser	530	535	540	

B1
Cont

Leu Gln Gly Arg Ser Glu Lys Gly Thr Leu Asp Ala Asn Leu Tyr Gln
545 550 555 560

Asn Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Asn Leu Thr Thr Ser
565 570 575

Gly Asp Val Gly Cys Thr Gln Met Asn Tyr Tyr Tyr Gly Met Cys Ser
580 585 590

Asn Pro Tyr Ser Glu Lys Pro Glu Trp Gln Met Gln Asn Ile Asp Lys
595 600 605

Ala Arg Ile Arg Gly Leu Glu Leu Thr Gly Arg Leu Asn Val Thr Lys
610 615 620

Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu Gly
625 630 635 640

Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr Gln
645 650 655

Pro Pro Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu Lys
660 665 670

Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Ala Lys
675 680 685

Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Arg Gly Thr Pro Leu
690 695 700

Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr Val
705 710 715 720

Phe Asp Met Tyr Gly Phe Tyr Lys Leu Ala Lys Asn Leu Thr Leu Arg
725 730 735

Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp Asp Ser
740 745 750

Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ala Val Asp Arg Asp
755 760 765

Gly Lys Gly Leu Asp Arg Tyr Arg Ala Ser Gly Arg Asn Tyr Ala Val
770 775 780

Ser Leu Asp Trp Lys Phe
785 790

B1
Cont